

# SEQUENCE LISTING

<110> Allen, Stephen  
 <120> Plant Cellulose Synthases  
 <130> BB1170 US CIP  
 <140>  
 <141>  
 <150> 60/092,844  
 <151> 1998-07-14  
 <150> PCT/US99/15871  
 <151> 1999-07-13  
 <150> 09/720383  
 <151> 2000-12-21  
 <160> 33  
 <170> Microsoft Office 97  
 <210> 1  
 <211> 1221  
 <212> DNA  
 <213> Hordeum vulgare

<400> 1  
 gcacgaggat attcttactg ggttttaaat gcaogcaaga gggttgatat caatctactg 60  
 catgccacca cgaccttggt tcaaggggtt tgcgccaatc aatctctctg accgtctcaa 120  
 tcaagttctc cgggtgggctc ttgggtcagt tgaaattctg tttagcagac attgtcctat 180  
 ctggtacaat tacggtgggc ggttgaaact tctggagagg atggcttaca tcaacacccat 240  
 tgtttatcca ataacatccc ttccacttat cgcctattgt gtgcttctg ctatctgtct 300  
 cctcaccaac aaatttatca ttcccgagat cagtaactat gctgggatgt tctttattct 360  
 tatgtttgcc tccatctttg ccacgggtat attggagctg cgatggagtg gtgtcggcac 420  
 cgaggactgg tggagaaacg agcagttctg gggtatttgt ggcacatctg cccatctttt 480  
 cgcagtggtc caggggtctgc tgaaggtgtt ggccgggatt gacaccaact tcacggttac 540  
 ctccaaggca aacgacgagg atggcgattt tgctgagtta tacgtgttca agtggaccag 600  
 tctctcatt cctccgacca ccgtccttgt gattaacctg gtgggcatgg tggcaggcat 660  
 atcatatgcc atcaacagcg gttaccagtc ttgggggtcca ctcttcggaa agctcttctt 720  
 ctcaatctgg gtgatcctcc atctctaccc ctctctcaag ggtctcatgg ggaagcagaa 780  
 ccgcacgcca accatcgta ttggttggtc catctccta gcctccatct tctccctcct 840  
 gtgggtgaag atcgacctt tcatatccga taccagaaa gccgtcgcca tggggcagtg 900  
 tggcgtcaac tgctgatcg cgccgaagag tatctgcccc cctcgtgtaa ataccggagg 960  
 ggggttgatg ggattttgtt gttgtagatg aagacggagt tttatgtaag ttattattgc 1020  
 cccttcgtgc tgagaagcac aaaccgtgaa gcctacgaaa cctgcagcgt acattgtgat 1080  
 tttttctcc tttcttttc atctgtgata cctgttggtt ctctttagag tatattatgt 1140  
 cagaacgtat ctatagttct atacacacta tgacaccaac tatttatata aggcagctgt 1200  
 tgcacaaact cttctgcaaa a 1221

<210> 2  
 <211> 304  
 <212> PRT  
 <213> Hordeum vulgare

<400> 2  
 His Glu Asp Ile Leu Thr Gly Phe Lys Met His Ala Arg Gly Trp Ile  
 1 5 10 15

09900237-070601

Sub  
B1

Ser Ile Tyr Cys Met Pro Pro Arg Pro Cys Phe Lys Gly Ser Ala Pro  
20 25 30

Ile Asn Leu Ser Asp Arg Leu Asn Gln Val Leu Arg Trp Ala Leu Gly  
35 40 45

Ser Val Glu Ile Leu Phe Ser Arg His Cys Pro Ile Trp Tyr Asn Tyr  
50 55 60

Gly Gly Arg Leu Lys Leu Leu Glu Arg Met Ala Tyr Ile Asn Thr Ile  
65 70 75 80

Val Tyr Pro Ile Thr Ser Leu Pro Leu Ile Ala Tyr Cys Val Leu Pro  
85 90 95

Ala Ile Cys Leu Leu Thr Asn Lys Phe Ile Ile Pro Glu Ile Ser Asn  
100 105 110

Tyr Ala Gly Met Phe Phe Ile Leu Met Phe Ala Ser Ile Phe Ala Thr  
115 120 125

Gly Ile Leu Glu Leu Arg Trp Ser Gly Val Gly Ile Glu Asp Trp Trp  
130 135 140

Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Thr Ser Ala His Leu Phe  
145 150 155 160

Ala Val Phe Gln Gly Leu Leu Lys Val Leu Ala Gly Ile Asp Thr Asn  
165 170 175

Phe Thr Val Thr Ser Lys Ala Asn Asp Glu Asp Gly Asp Phe Ala Glu  
180 185 190

Leu Tyr Val Phe Lys Trp Thr Ser Leu Leu Ile Pro Pro Thr Thr Val  
195 200 205

Leu Val Ile Asn Leu Val Gly Met Val Ala Gly Ile Ser Tyr Ala Ile  
210 215 220

Asn Ser Gly Tyr Gln Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe  
225 230 235 240

Ser Ile Trp Val Ile Leu His Leu Tyr Pro Phe Leu Lys Gly Leu Met  
245 250 255

Gly Lys Gln Asn Arg Thr Pro Thr Ile Val Ile Val Trp Ser Ile Leu  
260 265 270

Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Lys Ile Asp Pro Phe Ile  
275 280 285

Ser Asp Thr Gln Lys Ala Val Ala Met Gly Gln Cys Gly Val Asn Cys  
290 295 300

<210> 3  
<211> 3776  
<212> DNA  
<213> Zea mays

<400> 3  
gcgcgccgcg caggcgcaac gcaacaaagg gaaaccccag ccggaggagc aaaagctagc 60  
aagcgtgtcc cccccctcc ctactcccg tttcattcca tccccccca gacgccgcta 120  
ccgcccgcgc cgcacgcacg cttgccccgg gatctggaga tctggtagcg ccagggggat 180  
ggaggccagc gccgggctgg tcgcccggctc gcacaaccgg aacgagctcg tcgtcatccg 240  
ccgcgatggc gagccagggc cgaagcccat ggaccagcgg aacggccagg tgtgccagat 300  
ttgcggcgac gacgtggggc gcaaccccga cggggagccg ttcgtggcct gcaacgagt 360  
cgcttcccc atctgccggg actgctacga gtacgagcgc cgcgagggca cgcagaactg 420  
ccccagtgcc aagaccgcgt tcaagcgct caaggggtgc gcgcgcgtgc ccggggacga 480  
ggaggaggac ggcgtcgacg acctggagaa cgagttcaac tggagcgaca agcacgactc 540  
ccagtacctc gccgagtcga tgctccacgc ccacatgagc tacggccgcg gcgccgacct 600  
cgacggcgtg ccgcagccat tccaccccat ccccaatgtt cccctcctca ccaacggaca 660  
gatggtcgat gacatcccgc cggaccagca cgccttctgt cctcgttctg tgggtggcgg 720  
ggggaagagg attcaccctc tcccgtagc ggatcccaac cttcctgtgc aaccgaggtc 780  
tatggaccct tccaaggatc tcgcgcgata tggctacggg agcgtagcat ggaaggagag 840  
gatggagagc tggaaagcaga agcaggagag gatgcaccag acgaggaacg atggcggcgg 900  
cgatgatggt gatgatgcag atctaccact aatggatgaa gctagacagc cattgtccag 960  
aaagatcccg cttccttcaa gccaaatcaa cccctatagg atgattataa taattcggct 1020  
agtggttttg tgtttcttct tccactaccg agtgatgcac ccggtgcctg atgcatttgc 1080  
tttatggctc atatctgtga tctgtgaaat ttggtttgcc atgtcttga ttcttgacca 1140  
gtttccaaag tggtttccca tcgagaggga aacctatctt gaccggctga gtttaaggtt 1200  
tgacaaggaa gggcctcctt ctcaactcgc cctgttgat ttctttgtca gtacggttga 1260  
tcccttgaag gaacctccat tggctactgc taatactgtt ctatctatcc tttcgggtga 1320  
ttatccagtt gataaggttt catgctacgt ttctgatgat ggtgctgcca tgctgacatt 1380  
tgaagcattg tctgaaacat ctgaatttgc aaagaaatgg gttcctttct gcaaaagata 1440  
tagccttgag cctcgtgctc cagagtggta cttccaacag aagatagact acctgaaaga 1500  
caaggtggcg ccaaactttg tttagaagc gagagcaatg aagagagagt atgaggaatt 1560  
caaggtcaga atcaatgcct tggttgctaa agcccaaaag gttcctgagg aaggttgac 1620  
aatgcaggat ggaactccat ggcccggaaa taatgtccgt gatcatcctg gaatgattca 1680  
ggttttccct ggtcaaagtg gtggccatga tgtggaagga aatgagctgc ctgattggt 1740  
ttatgtttca agagaaaaac ggccaggcta caaccatcac aagaaggctg gtgctatgaa 1800  
tgcatgtgct cgagtctctg ctgtactaac taatgtcctt tatttgctga acttgattg 1860  
tgatcactat atcaataata gtaaggctat aaaggaagca atgtgtttta tgatggatcc 1920  
tttgcttgga aagaaagttt gctatgtgca gtttccctca agatttgatg ggattgatcg 1980  
ccatgatcga tatgctaaca gaaatgttgt ctttttogat atcaacatga aaggtttgga 2040  
tggtatccag ggcccaattt atgtgggtac tctgtgtgtc tcagaaggc gccatggtt 2100  
tggtacgat gctcccaaaa caaagaagcc accatcaaga acttgcaact gctggccaaa 2160  
gtggtgcatt tgctgttgct gttttggtaa caggaagacc aagaagaaga ccaagacctc 2220  
taaacctaaa tttgagaaga taaagaaact ttttaagaaa aaggaaaatc aagcccctgc 2280  
atatgctctt ggtgaaattg atgaagccgc tccaggagct gaaaatgaaa aggctagtat 2340  
tgtaaatcaa cagaagttgg aaaagaaatt tggccagctc tcagtttttg ttgcatccac 2400  
acttcttgag aatggtggaa ccctgaagag tgccagtcga gcttctcttc tgaaggaaagc 2460  
tatacatgtc atcagttgtg gatatgaaga caaacaggc tggggaaaag atattggtt 2520  
gatttatgga tcagtcacag aagatattct tactgggtt aagatgcact gccatggtt 2580  
gcggtcaatt tactgcatac ctaaacgggc cgcttcaaaa ggttccgcac ctctcaatct 2640  
ttccgatcgt cttcaccagg ttcttcgggt ggctcttggt tcaattgaaa ttttcttcag 2700  
caaccactgc cctctctggt atgggtatgg tgggtgacta aagttcctgg aaaggttttc 2760  
gtacattaac tccatcgat acccttgga atctatccc ctcttgccct attgcacatt 2820  
gcctgccatc tgcttgctga cagggaat tttgctacg gatcttaaca atgttgccag 2880  
cctctggttc atgtcactt tcatctgcat ttttgctacg agcatcctgg aaatgagatg 2940  
gagtggtgta ggcactgat actggtggag aaacgagcag ttttgggtca ttggagcgt 3000  
gtcttcacat ctctttgctg tgttccaggg actcctcaag gtcatagctg gtgtagacac 3060  
gagcttcaat gtgacatcca agggcggaga cgacgaggag ttctcagagc tgtacacatt 3120  
caaattggacg acccttctga tacctccgac aacctgctc ctactgaact tcattggagt 3180  
ggtagctggc atctccaatg cgatcaacaa cggatatgaa tcatggggcc ccctgttcgg 3240  
gaagctcttc tttgcathtt ggggtgatcg ccatctttac ccgttctctc agggctctgg 3300  
tgaggaggcag aacaggacgc caacgattgt cattgtctgg tccatcctcc tggcttcgat 3360  
cttctcgctg ctttgggtcc ggatcgaccc gttccttgcg aaggatgatg gtccctgtt 3420  
ggaggagtgt ggtctggatt gcaactagga ggtcagcacg tggacttccc cgtcagtggt 3480  
tggtcgaaga agtatttttg cagatgtttt gtgcccata ttttttttc aatttttgc 3540

cctctgtaga tagaaacaag gggagaaggg gaaaaaaagt acttgtattt cttttgttcc 3600  
atggtggtgg tgggtggtggg cggctcagcc tcgtgagtgc agtattgggc aaaccggagg 3660  
ctgcggcaac cttgtgcagt tcggccacga atatactagg gaagatcgcg accaatcaat 3720  
caatcgatga cggagttcaa ttgttcagca aaaaaaaaaa aaaaaaaaaa aaaaaa 3776

<210> 4  
<211> 1148  
<212> PRT  
<213> Zea mays

<400> 4  
Arg Ala Ala Gln Ala Gln Arg Asn Lys Gly Lys Pro Gln Pro Glu Glu  
1 5 10 15  
Gln Lys Leu Ala Ser Val Ser Leu Pro Leu Pro His Ser Arg Phe Ile  
20 25 30  
Pro Phe Pro Pro Arg Arg Arg Tyr Arg Arg Arg Arg Thr His Ala Cys  
35 40 45  
Pro Gly Ile Trp Arg Ser Gly Ser Ala Arg Gly Met Glu Ala Ser Ala  
50 55 60  
Gly Leu Val Ala Gly Ser His Asn Arg Asn Glu Leu Val Val Ile Arg  
65 70 75 80  
Arg Asp Gly Glu Pro Gly Pro Lys Pro Met Asp Gln Arg Asn Gly Gln  
85 90 95  
Val Cys Gln Ile Cys Gly Asp Asp Val Gly Arg Asn Pro Asp Gly Glu  
100 105 110  
Pro Phe Val Ala Cys Asn Glu Cys Ala Phe Pro Ile Cys Arg Asp Cys  
115 120 125  
Tyr Glu Tyr Glu Arg Arg Glu Gly Thr Gln Asn Cys Pro Gln Cys Lys  
130 135 140  
Thr Arg Phe Lys Arg Leu Lys Gly Cys Ala Arg Val Pro Gly Asp Glu  
145 150 155 160  
Glu Glu Asp Gly Val Asp Asp Leu Glu Asn Glu Phe Asn Trp Ser Asp  
165 170 175  
Lys His Asp Ser Gln Tyr Leu Ala Glu Ser Met Leu His Ala His Met  
180 185 190  
Ser Tyr Gly Arg Gly Ala Asp Leu Asp Gly Val Pro Gln Pro Phe His  
195 200 205  
Pro Ile Pro Asn Val Pro Leu Leu Thr Asn Gly Gln Met Val Asp Asp  
210 215 220  
Ile Pro Pro Asp Gln His Ala Leu Val Pro Ser Phe Val Gly Gly Gly  
225 230 235 240  
Gly Lys Arg Ile His Pro Leu Pro Tyr Ala Asp Pro Asn Leu Pro Val  
245 250 255

Gln	Pro	Arg	Ser	Met	Asp	Pro	Ser	Lys	Asp	Leu	Ala	Ala	Tyr	Gly	Tyr		
			260					265					270				
Gly	Ser	Val	Ala	Trp	Lys	Glu	Arg	Met	Glu	Ser	Trp	Lys	Gln	Lys	Gln		
		275					280					285					
Glu	Arg	Met	His	Gln	Thr	Arg	Asn	Asp	Gly	Gly	Gly	Asp	Asp	Gly	Asp		
	290					295					300						
Asp	Ala	Asp	Leu	Pro	Leu	Met	Asp	Glu	Ala	Arg	Gln	Pro	Leu	Ser	Arg		
305					310					315					320		
Lys	Ile	Pro	Leu	Pro	Ser	Ser	Gln	Ile	Asn	Pro	Tyr	Arg	Met	Ile	Ile		
			325						330					335			
Ile	Ile	Arg	Leu	Val	Val	Leu	Cys	Phe	Phe	Phe	His	Tyr	Arg	Val	Met		
		340						345					350				
His	Pro	Val	Pro	Asp	Ala	Phe	Ala	Leu	Trp	Leu	Ile	Ser	Val	Ile	Cys		
		355					360					365					
Glu	Ile	Trp	Phe	Ala	Met	Ser	Trp	Ile	Leu	Asp	Gln	Phe	Pro	Lys	Trp		
	370					375					380						
Phe	Pro	Ile	Glu	Arg	Glu	Thr	Tyr	Leu	Asp	Arg	Leu	Ser	Leu	Arg	Phe		
385					390					395					400		
Asp	Lys	Glu	Gly	His	Pro	Ser	Gln	Leu	Ala	Pro	Val	Asp	Phe	Phe	Val		
				405					410					415			
Ser	Thr	Val	Asp	Pro	Leu	Lys	Glu	Pro	Pro	Leu	Val	Thr	Ala	Asn	Thr		
			420					425					430				
Val	Leu	Ser	Ile	Leu	Ser	Val	Asp	Tyr	Pro	Val	Asp	Lys	Val	Ser	Cys		
		435					440					445					
Tyr	Val	Ser	Asp	Asp	Gly	Ala	Ala	Met	Leu	Thr	Phe	Glu	Ala	Leu	Ser		
	450					455					460						
Glu	Thr	Ser	Glu	Phe	Ala	Lys	Lys	Trp	Val	Pro	Phe	Cys	Lys	Arg	Tyr		
465					470					475					480		
Ser	Leu	Glu	Pro	Arg	Ala	Pro	Glu	Trp	Tyr	Phe	Gln	Gln	Lys	Ile	Asp		
				485					490					495			
Tyr	Leu	Lys	Asp	Lys	Val	Ala	Pro	Asn	Phe	Val	Arg	Glu	Arg	Arg	Ala		
			500					505					510				
Met	Lys	Arg	Glu	Tyr	Glu	Glu	Phe	Lys	Val	Arg	Ile	Asn	Ala	Leu	Val		
		515					520					525					
Ala	Lys	Ala	Gln	Lys	Val	Pro	Glu	Glu	Gly	Trp	Thr	Met	Gln	Asp	Gly		
	530					535					540						
Thr	Pro	Trp	Pro	Gly	Asn	Asn	Val	Arg	Asp	His	Pro	Gly	Met	Ile	Gln		
545					550					555					560		
Val	Phe	Leu	Gly	Gln	Ser	Gly	Gly	His	Asp	Val	Glu	Gly	Asn	Glu	Leu		
				565					570					575			

Pro	Arg	Leu	Val	Tyr	Val	Ser	Arg	Glu	Lys	Arg	Pro	Gly	Tyr	Asn	His		
			580					585					590				
His	Lys	Lys	Ala	Gly	Ala	Met	Asn	Ala	Leu	Val	Arg	Val	Ser	Ala	Val		
		595					600					605					
Leu	Thr	Asn	Ala	Pro	Tyr	Leu	Leu	Asn	Leu	Asp	Cys	Asp	His	Tyr	Ile		
	610					615					620						
Asn	Asn	Ser	Lys	Ala	Ile	Lys	Glu	Ala	Met	Cys	Phe	Met	Met	Asp	Pro		
625					630					635					640		
Leu	Leu	Gly	Lys	Lys	Val	Cys	Tyr	Val	Gln	Phe	Pro	Gln	Arg	Phe	Asp		
				645					650					655			
Gly	Ile	Asp	Arg	His	Asp	Arg	Tyr	Ala	Asn	Arg	Asn	Val	Val	Phe	Phe		
			660					665						670			
Asp	Ile	Asn	Met	Lys	Gly	Leu	Asp	Gly	Ile	Gln	Gly	Pro	Ile	Tyr	Val		
		675					680					685					
Gly	Thr	Gly	Cys	Val	Phe	Arg	Arg	Gln	Ala	Leu	Tyr	Gly	Tyr	Asp	Ala		
	690					695						700					
Pro	Lys	Thr	Lys	Lys	Pro	Pro	Ser	Arg	Thr	Cys	Asn	Cys	Trp	Pro	Lys		
705					710					715					720		
Trp	Cys	Ile	Cys	Cys	Cys	Cys	Phe	Gly	Asn	Arg	Lys	Thr	Lys	Lys	Lys		
				725					730					735			
Thr	Lys	Thr	Ser	Lys	Pro	Lys	Phe	Glu	Lys	Ile	Lys	Lys	Leu	Phe	Lys		
			740					745					750				
Lys	Lys	Glu	Asn	Gln	Ala	Pro	Ala	Tyr	Ala	Leu	Gly	Glu	Ile	Asp	Glu		
		755					760					765					
Ala	Ala	Pro	Gly	Ala	Glu	Asn	Glu	Lys	Ala	Ser	Ile	Val	Asn	Gln	Gln		
	770					775					780						
Lys	Leu	Glu	Lys	Lys	Phe	Gly	Gln	Ser	Ser	Val	Phe	Val	Ala	Ser	Thr		
785					790					795					800		
Leu	Leu	Glu	Asn	Gly	Gly	Thr	Leu	Lys	Ser	Ala	Ser	Pro	Ala	Ser	Leu		
			805						810					815			
Leu	Lys	Glu	Ala	Ile	His	Val	Ile	Ser	Cys	Gly	Tyr	Glu	Asp	Lys	Thr		
			820					825					830				
Gly	Trp	Gly	Lys	Asp	Ile	Gly	Trp	Ile	Tyr	Gly	Ser	Val	Thr	Glu	Asp		
		835					840					845					
Ile	Leu	Thr	Gly	Phe	Lys	Met	His	Cys	His	Gly	Trp	Arg	Ser	Ile	Tyr		
	850					855					860						
Cys	Ile	Pro	Lys	Arg	Ala	Ala	Phe	Lys	Gly	Ser	Ala	Pro	Leu	Asn	Leu		
865					870					875					880		
Ser	Asp	Arg	Leu	His	Gln	Val	Leu	Arg	Trp	Ala	Leu	Gly	Ser	Ile	Glu		
				885					890						895		

09900237.070601

Ile Phe Phe Ser Asn His Cys Pro Leu Trp Tyr Gly Tyr Gly Gly Gly  
900 905 910

Leu Lys Phe Leu Glu Arg Phe Ser Tyr Ile Asn Ser Ile Val Tyr Pro  
915 920 925

Trp Thr Ser Ile Pro Leu Leu Ala Tyr Cys Thr Leu Pro Ala Ile Cys  
930 935 940

Leu Leu Thr Gly Lys Phe Ile Thr Pro Glu Leu Asn Asn Val Ala Ser  
945 950 955 960

Leu Trp Phe Met Ser Leu Phe Ile Cys Ile Phe Ala Thr Ser Ile Leu  
965 970 975

Glu Met Arg Trp Ser Gly Val Gly Ile Asp Asp Trp Trp Arg Asn Glu  
980 985 990

Gln Phe Trp Val Ile Gly Gly Val Ser Ser His Leu Phe Ala Val Phe  
995 1000 1005

Gln Gly Leu Leu Lys Val Ile Ala Gly Val Asp Thr Ser Phe Thr Val  
1010 1015 1020

Thr Ser Lys Gly Gly Asp Asp Glu Glu Phe Ser Glu Leu Tyr Thr Phe  
1025 1030 1035 1040

Lys Trp Thr Thr Leu Leu Ile Pro Pro Thr Thr Leu Leu Leu Leu Asn  
1045 1050 1055

Phe Ile Gly Val Val Ala Gly Ile Ser Asn Ala Ile Asn Asn Gly Tyr  
1060 1065 1070

Glu Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe Ala Phe Trp Val  
1075 1080 1085

Ile Val His Leu Tyr Pro Phe Leu Lys Gly Leu Val Gly Arg Gln Asn  
1090 1095 1100

Arg Thr Pro Thr Ile Val Ile Val Trp Ser Ile Leu Leu Ala Ser Ile  
1105 1110 1115 1120

Phe Ser Leu Leu Trp Val Arg Ile Asp Pro Phe Leu Ala Lys Asp Asp  
1125 1130 1135

Gly Pro Leu Leu Glu Glu Cys Gly Leu Asp Cys Asn  
1140 1145

<210> 5  
<211> 1189  
<212> DNA  
<213> Zea mays

<400> 5  
gcacgagacc gagtggggcaggagattgg gtggatctat gggtcggtga cagaggatat 60  
cctgacgggg ttcaagatgc actgccgggg gtggaagtcc gtgtactgca cgccgacacg 120  
gccggcggtc aaggggtcgg cgcccatcaa cttgtctgat cgtctccacc aggtgctgcg 180  
ctgggcgctg gggtcctgag agatcttcat gagccgccac tgcccgctct ggtacgccta 240  
cggcgccggg ctcaagtggc tggagcgctt cgcctacacc aacaccatcg tgtaccctt 300  
cacctccatc ccgctcctcg cctactgcac catccccgcc gtctgctgc tcaccggcaa 360

```

gttcatcatt cccacgctga acaacctcgc cagcatctgg ttcacgcgc tcttctgtc 420
catcatcgcg acgagcgctc tggagctgcg gtggagcggg gtgagcatcg aggactgggtg 480
gcgcaacgag cagttctggg tcatcggcgg cgtgtccgcg catctcttcg ccgtgttcca 540
gggcttcctc aaggttctgg gcggcggtga caccagcttc accgtcacct ccaaggcggc 600
cggcgacgag gccgacgcct tcggggacct ctacctcttc aagtggacca ccctgctggt 660
gccccccacc acgctcatca tcatcaacat ggtgggcatc gtggccggcg tgtccgacgc 720
cgtcaacaac ggctacggct cctggggccc gctcttcggc aagctcttct tctccttctg 780
ggtcatcgtc cacctctacc cgttcctcaa ggggctcatg gggaggcaga accggacgcc 840
caccatcgtc gtgctctggt ccatacctct cgcctccatc ttctcgctcg tctgggtcag 900
gatcgacccg tttatcccgaggccaagg ccccatcctc aagccatgcg gactcgagt 960
ctgagctcac ctagctacct tcttggttga tgtacggacg ccgccgtgcg ttgggacata 1020
caggcacttt tgggocaggc tactcatggt cgactttttt ttttaattttg tacaagattt 1080
gtgatcgagt gactgagtga gacagagtgt tgggtgtaag aactgtgatg gaattcactc 1140
aaattaatgg acattttttt tcttcaactg caaaaaaaaa aaaaaaaaaa 1189

```

<210> 6  
 <211> 320  
 <212> PRT  
 <213> Zea mays

<400> 6

His	Glu	Thr	Glu	Trp	Gly	Lys	Glu	Ile	Gly	Trp	Ile	Tyr	Gly	Ser	Val
1				5					10					15	
Thr	Glu	Asp	Ile	Leu	Thr	Gly	Phe	Lys	Met	His	Cys	Arg	Gly	Trp	Lys
			20					25					30		
Ser	Val	Tyr	Cys	Thr	Pro	Thr	Arg	Pro	Ala	Phe	Lys	Gly	Ser	Ala	Pro
		35					40					45			
Ile	Asn	Leu	Ser	Asp	Arg	Leu	His	Gln	Val	Leu	Arg	Trp	Ala	Leu	Gly
	50					55					60				
Ser	Val	Glu	Ile	Phe	Met	Ser	Arg	His	Cys	Pro	Leu	Trp	Tyr	Ala	Tyr
	65				70					75					80
Gly	Gly	Arg	Leu	Lys	Trp	Leu	Glu	Arg	Phe	Ala	Tyr	Thr	Asn	Thr	Ile
				85					90					95	
Val	Tyr	Pro	Phe	Thr	Ser	Ile	Pro	Leu	Leu	Ala	Tyr	Cys	Thr	Ile	Pro
			100					105					110		
Ala	Val	Cys	Leu	Leu	Thr	Gly	Lys	Phe	Ile	Ile	Pro	Thr	Leu	Asn	Asn
		115					120					125			
Leu	Ala	Ser	Ile	Trp	Phe	Ile	Ala	Leu	Phe	Leu	Ser	Ile	Ile	Ala	Thr
	130					135					140				
Ser	Val	Leu	Glu	Leu	Arg	Trp	Ser	Gly	Val	Ser	Ile	Glu	Asp	Trp	Trp
	145				150					155				160	
Arg	Asn	Glu	Gln	Phe	Trp	Val	Ile	Gly	Gly	Val	Ser	Ala	His	Leu	Phe
				165					170					175	
Ala	Val	Phe	Gln	Gly	Phe	Leu	Lys	Val	Leu	Gly	Gly	Val	Asp	Thr	Ser
			180				185						190		
Phe	Thr	Val	Thr	Ser	Lys	Ala	Ala	Gly	Asp	Glu	Ala	Asp	Ala	Phe	Gly
		195					200					205			



Asp Leu Tyr Leu Phe Lys Trp Thr Thr Leu Leu Val Pro Pro Thr Thr  
 210 215 220  
 Leu Ile Ile Ile Asn Met Val Gly Ile Val Ala Gly Val Ser Asp Ala  
 225 230 235 240  
 Val Asn Asn Gly Tyr Gly Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe  
 245 250 255  
 Phe Ser Phe Trp Val Ile Val His Leu Tyr Pro Phe Leu Lys Gly Leu  
 260 265 270  
 Met Gly Arg Gln Asn Arg Thr Pro Thr Ile Val Val Leu Trp Ser Ile  
 275 280 285  
 Leu Leu Ala Ser Ile Phe Ser Leu Val Trp Val Arg Ile Asp Pro Phe  
 290 295 300  
 Ile Pro Lys Ala Lys Gly Pro Ile Leu Lys Pro Cys Gly Val Glu Cys  
 305 310 315 320

<210> 7  
 <211> 3786  
 <212> DNA  
 <213> Zea mays

<400> 7  
 ccacagctca tataccaaga gccggagcag cttagcgcag cccagagcgg cgccgcgcc 60  
 agcacaaccc ccaccgccca cagccgcgtg cgcgtgtgag cggtcgccgc ggccgggaga 120  
 ccagaggagg ggaggactac gtgcatttcg ctgtgccgcc gccgcggggt tcgtgcgcga 180  
 gcgagatccg gcggggcggg gcggggggcc tgagatggag gctagcgcgg ggctggtggc 240  
 cggtctgcat aaccggaacg agctggttgt gatccgccgc gaccgcgagt cgggagccgc 300  
 gggcgggcgc gcggcgccgc gggcgagggc gccgtgccag atatgcggcg acgaggtcgg 360  
 ggtgggcttc gacggggagc ccttcgtggc gtgcaacgag tgcgccttcc cgtctgccg 420  
 cgcctgctac gagtacgagc gccgcgaggg ctgcgaagcg tgcccgcagt gcaggaccgc 480  
 ctacaagcgc ctcaagggtt gcccgcgggt ggccggcgac gaggaggagg acggcgctcg 540  
 cgacctggag ggcgagttcg gcctgcagga cggcgccgcc caccaggacg accgcagta 600  
 cgtcgccgag tccatgctca gggcgagat gagctacggc cgcggcgggc acgcgcaccc 660  
 cggcttcagc cccgtcccca acgtgccgct cctcaccaac ggccagatgg ttgatgacat 720  
 cccgcgggag cagcacgcgc tcgtgccgtc ctacatgagc ggccggcgggc gcgggggcaa 780  
 gaggatccac ccgtccctt tcgcagatcc caaccttcca gtgcaaccga gatccatgga 840  
 cccgtccaag gatctggccg cctacggata tggcagcgtg gcctggaagg agagaatgga 900  
 gggctggaag cagaagcagg agcgctgca gcatgtcagg agcgagggtg gcggtgattg 960  
 ggatggcgac gatgcagatc tgccactaat ggatgaagct aggcagccat tgtccagaaa 1020  
 agtccctata tcatcaagcc gaattaatcc ctacaggatg attatcgtta tccggttgtt 1080  
 ggttttgggt ttcttcttcc actaccgagt gatgcattcc gcgaaagatg catttgcatt 1140  
 gtggctcata tctgtaattc gtgaaatctg gtttgcgatg tcctggattc ttgatcagtt 1200  
 cccaaagtgg cttccaatcg agagagagac ttacctggac cgtttgtcac taaggtttga 1260  
 caaggaaggc caaccctctc agcttgctcc aatcgacttc tttgtcagta cgtttgatcc 1320  
 cacaaaggaa cctcccttgg tcacagcgaa cactgtcctt tccatccttt ctgtggatta 1380  
 tccggttgag aaggtctcct gctatgttcc tgatgatggg gctgcaatgc ttacgtttga 1440  
 agcattgtct gaaacatctg aatttgcaaa gaaatgggtt cttttcagca aaaagttaa 1500  
 tatcgagcct cgtgctcctg agtggactt ccaacagaag atagactacc tgaaagacaa 1560  
 ggttgctgct tcatttggtt gggagaggag ggcgatgaag agagaatacg aggaattcaa 1620  
 ggtaaggatc aatgccttgg ttgcaaaagc ccaaaagggt cctgaggaag gatggacaat 1680  
 gcaagatgga agcccttggc ctggaaacaa cgtacgcgat catcctggaa tgattcaggt 1740  
 attccttggc caaagtggcg gtctgtatgt ggaaggaaat gagttgcctc gcctggttta 1800  
 tgtctcgaga gaaaagaggc caggttataa ccatcacaag aaggctgggt ccatgaatgc 1860  
 actggtccgt gtctctgctg tcttatcaaa tgctgcatac ctattgaact tggactgtga 1920  
 tcactacatc aacaatagca aggccataaa agaggctatg tgtttcatga tggatccttt 1980

```

ggtggggaag aaagtgtgct atgtacagtt cctcagagg tttgatggta ttgacaaaaa 2040
tgatcgatac gctaacagga acgttgtctt ttttgacatc aacatgaaag gtttgacagg 2100
tattcaagga cccatttatg tgggtactgg atgtgttttc agacggcagg cactgtatgg 2160
ttatgatgct cctaaaacga agaagccacc atcaagaact tgcaactgct ggcccaagtg 2220
gtgcctctct tgctgctgca gcaggaacaa gaataaaaaa aagactacaa aaccaaagac 2280
ggagaagaag aaaagattat ttttcaagaa agcagaaaac ccatctcctg catatgcttt 2340
gggtgaaatt gatgaaggtg ctccaggtgc tgatatcgag aaggccggaa tcgtaaataca 2400
acagaaacta gagaagaaat ttgggcagtc ttctgttttt gtcgcatcaa cacttcttga 2460
gaacggaggg accctgaaga gcgcaagtcc agcttctctt ctgaaggaag ctatacatgt 2520
tatcagctgc ggctacgaag acaagaccga ctggggaaaa gagattggct ggatttacgg 2580
atcgatcaca gaggatatct tgactggatt taagatgcac tgccatggct ggcggtctat 2640
ttactgcatc ccgaagcggc ctgcattcaa aggttctgcg cctctgaacc tttccgaccg 2700
tcttcaccag gtccttcgct gggcccttgg gtccgtcgaa attttcttca gcaagcactg 2760
cccactttgg tacggatacg ggggggggct aaaattcctg gaaaggtttt cttatatcaa 2820
ctccatcggt tatccctgga cgtccattcc tctcctggct tactgtacct tgccctgcca 2880
ctgcctgctc acggggaagt ttatcacacc agagcttacc aatgtcgcca gtatctgggt 2940
catggcactt ttcattctga tctccgtgac cggcatcctg gaaatgaggt ggagtggcgt 3000
ggccatcgac gactggtgga ggaacgagca gttctgggtc atcggaggcg tttcggcgca 3060
tctgttcgcg gtgttcagg gctgctgaa ggtgttcgcc ggcacgcaca cgagcttcac 3120
cgtgacgtcg aaggccgggg acgacgagga gttctcggag ctgtacacgt tcaagtggac 3180
caccctgctg atacccccga ccacgctcct cctgctgaac ttcacggggg tgggtggccgg 3240
gatctcgaac gcgatcaaca acgggtacga gtctggtggc cccctgttcg ggaagctctt 3300
cttcgccttc tgggtgatcg tccacctgta cccgttcctc aagggtctgg tggggaggca 3360
gaacaggacg ccgacgatcg tcatcgtctg gtccatcctg ctggcctcga tcttctcgtc 3420
cctgtgggtc cgcgtcgacc cgttctcgc caagagcaac ggcccgctcc tggaggagtg 3480
tggcctggac tgcaactgaa gtggggggcc cctgtcactc gaagtctgtg cacgggcgaa 3540
ttacgcctga ttttttgttg ttgttgttgt tgggaattctt tgctgtagat agaaaccaca 3600
tgtccacggc atctctgctg tgtccattgg agcaggagag aggtgcctgc tgctgtttgt 3660
tgagtaaatt aaaagtttta aagttatata gtgatgcaca ttccagtgcc cagtgtattc 3720
cctttttaca gtctgtatat tagcgacaaa ggacatatgt gttaggagtt tgattctttt 3780
gtaaaa 3786

```

```

<210> 8
<211> 1165
<212> PRT
<213> Zea mays

```

```

<400> 8
His Ser Ser Tyr Thr Lys Ser Arg Ser Ser Leu Ala Gln Pro Arg Ala
 1             5             10             15

Ala Pro Arg Gln Ala Gln Pro Pro Pro Ala Thr Ala Ala Cys Ala Cys
 20             25             30

Glu Arg Ser Pro Arg Pro Gly Asp Gln Arg Arg Gly Gly Leu Arg Ala
 35             40             45

Phe Arg Cys Ala Ala Ala Ala Gly Phe Val Arg Glu Arg Asp Pro Ala
 50             55             60

Gly Arg Gly Gly Gly Pro Glu Met Glu Ala Ser Ala Gly Leu Val Ala
 65             70             75             80

Gly Ser His Asn Arg Asn Glu Leu Val Val Ile Arg Arg Asp Arg Glu
 85             90             95

Ser Gly Ala Ala Gly Gly Gly Ala Ala Arg Arg Ala Glu Ala Pro Cys
100             105             110

```

Gln	Ile	Cys	Gly	Asp	Glu	Val	Gly	Val	Gly	Phe	Asp	Gly	Glu	Pro	Phe	
		115					120					125				
Val	Ala	Cys	Asn	Glu	Cys	Ala	Phe	Pro	Val	Cys	Arg	Ala	Cys	Tyr	Glu	
	130					135					140					
Tyr	Glu	Arg	Arg	Glu	Gly	Ser	Gln	Ala	Cys	Pro	Gln	Cys	Arg	Thr	Arg	
145					150					155					160	
Tyr	Lys	Arg	Leu	Lys	Gly	Cys	Pro	Arg	Val	Ala	Gly	Asp	Glu	Glu	Glu	
			165						170					175		
Asp	Gly	Val	Asp	Asp	Leu	Glu	Gly	Glu	Phe	Gly	Leu	Gln	Asp	Gly	Ala	
			180					185					190			
Ala	His	Glu	Asp	Asp	Pro	Gln	Tyr	Val	Ala	Glu	Ser	Met	Leu	Arg	Ala	
		195					200					205				
Gln	Met	Ser	Tyr	Gly	Arg	Gly	Gly	Asp	Ala	His	Pro	Gly	Phe	Ser	Pro	
	210					215					220					
Val	Pro	Asn	Val	Pro	Leu	Leu	Thr	Asn	Gly	Gln	Met	Val	Asp	Asp	Ile	
225					230					235					240	
Pro	Pro	Glu	Gln	His	Ala	Leu	Val	Pro	Ser	Tyr	Met	Ser	Gly	Gly	Gly	
				245					250					255		
Gly	Gly	Gly	Lys	Arg	Ile	His	Pro	Leu	Pro	Phe	Ala	Asp	Pro	Asn	Leu	
			260					265					270			
Pro	Val	Gln	Pro	Arg	Ser	Met	Asp	Pro	Ser	Lys	Asp	Leu	Ala	Ala	Tyr	
		275					280					285				
Gly	Tyr	Gly	Ser	Val	Ala	Trp	Lys	Glu	Arg	Met	Glu	Gly	Trp	Lys	Gln	
	290					295					300					
Lys	Gln	Glu	Arg	Leu	Gln	His	Val	Arg	Ser	Glu	Gly	Gly	Gly	Asp	Trp	
305					310					315					320	
Asp	Gly	Asp	Asp	Ala	Asp	Leu	Pro	Leu	Met	Asp	Glu	Ala	Arg	Gln	Pro	
				325					330					335		
Leu	Ser	Arg	Lys	Val	Pro	Ile	Ser	Ser	Ser	Arg	Ile	Asn	Pro	Tyr	Arg	
			340					345					350			
Met	Ile	Ile	Val	Ile	Arg	Leu	Val	Val	Leu	Gly	Phe	Phe	Phe	His	Tyr	
		355					360					365				
Arg	Val	Met	His	Pro	Ala	Lys	Asp	Ala	Phe	Ala	Leu	Trp	Leu	Ile	Ser	
		370				375					380					
Val	Ile	Cys	Glu	Ile	Trp	Phe	Ala	Met	Ser	Trp	Ile	Leu	Asp	Gln	Phe	
385					390					395					400	
Pro	Lys	Trp	Leu	Pro	Ile	Glu	Arg	Glu	Thr	Tyr	Leu	Asp	Arg	Leu	Ser	
				405					410					415		
Leu	Arg	Phe	Asp	Lys	Glu	Gly	Gln	Pro	Ser	Gln	Leu	Ala	Pro	Ile	Asp	
			420					425					430			

Phe	Phe	Val	Ser	Thr	Val	Asp	Pro	Thr	Lys	Glu	Pro	Pro	Leu	Val	Thr	
		435					440					445				
Ala	Asn	Thr	Val	Leu	Ser	Ile	Leu	Ser	Val	Asp	Tyr	Pro	Val	Glu	Lys	
	450					455					460					
Val	Ser	Cys	Tyr	Val	Ser	Asp	Asp	Gly	Ala	Ala	Met	Leu	Thr	Phe	Glu	
465					470					475					480	
Ala	Leu	Ser	Glu	Thr	Ser	Glu	Phe	Ala	Lys	Lys	Trp	Val	Pro	Phe	Ser	
				485					490					495		
Lys	Lys	Phe	Asn	Ile	Glu	Pro	Arg	Ala	Pro	Glu	Trp	Tyr	Phe	Gln	Gln	
			500					505					510			
Lys	Ile	Asp	Tyr	Leu	Lys	Asp	Lys	Val	Ala	Ala	Ser	Phe	Val	Arg	Glu	
		515					520					525				
Arg	Arg	Ala	Met	Lys	Arg	Glu	Tyr	Glu	Glu	Phe	Lys	Val	Arg	Ile	Asn	
	530					535					540					
Ala	Leu	Val	Ala	Lys	Ala	Gln	Lys	Val	Pro	Glu	Glu	Gly	Trp	Thr	Met	
545					550					555					560	
Gln	Asp	Gly	Ser	Pro	Trp	Pro	Gly	Asn	Asn	Val	Arg	Asp	His	Pro	Gly	
				565					570					575		
Met	Ile	Gln	Val	Phe	Leu	Gly	Gln	Ser	Gly	Gly	Arg	Asp	Val	Glu	Gly	
			580					585					590			
Asn	Glu	Leu	Pro	Arg	Leu	Val	Tyr	Val	Ser	Arg	Glu	Lys	Arg	Pro	Gly	
		595					600					605				
Tyr	Asn	His	His	Lys	Lys	Ala	Gly	Ala	Met	Asn	Ala	Leu	Val	Arg	Val	
	610					615					620					
Ser	Ala	Val	Leu	Ser	Asn	Ala	Ala	Tyr	Leu	Leu	Asn	Leu	Asp	Cys	Asp	
625					630					635					640	
His	Tyr	Ile	Asn	Asn	Ser	Lys	Ala	Ile	Lys	Glu	Ala	Met	Cys	Phe	Met	
			645						650					655		
Met	Asp	Pro	Leu	Val	Gly	Lys	Lys	Val	Cys	Tyr	Val	Gln	Phe	Pro	Gln	
			660					665					670			
Arg	Phe	Asp	Gly	Ile	Asp	Lys	Asn	Asp	Arg	Tyr	Ala	Asn	Arg	Asn	Val	
		675					680					685				
Val	Phe	Phe	Asp	Ile	Asn	Met	Lys	Gly	Leu	Asp	Gly	Ile	Gln	Gly	Pro	
	690					695					700					
Ile	Tyr	Val	Gly	Thr	Gly	Cys	Val	Phe	Arg	Arg	Gln	Ala	Leu	Tyr	Gly	
705					710					715					720	
Tyr	Asp	Ala	Pro	Lys	Thr	Lys	Lys	Pro	Pro	Ser	Arg	Thr	Cys	Asn	Cys	
				725					730					735		
Trp	Pro	Lys	Trp	Cys	Leu	Ser	Cys	Cys	Cys	Ser	Arg	Asn	Lys	Asn	Lys	
			740					745					750			

Lys	Lys	Thr	Thr	Lys	Pro	Lys	Thr	Glu	Lys	Lys	Lys	Arg	Leu	Phe	Phe		
		755					760					765					
Lys	Lys	Ala	Glu	Asn	Pro	Ser	Pro	Ala	Tyr	Ala	Leu	Gly	Glu	Ile	Asp		
		770				775					780						
Glu	Gly	Ala	Pro	Gly	Ala	Asp	Ile	Glu	Lys	Ala	Gly	Ile	Val	Asn	Gln		
785					790					795					800		
Gln	Lys	Leu	Glu	Lys	Lys	Phe	Gly	Gln	Ser	Ser	Val	Phe	Val	Ala	Ser		
				805					810					815			
Thr	Leu	Leu	Glu	Asn	Gly	Gly	Thr	Leu	Lys	Ser	Ala	Ser	Pro	Ala	Ser		
			820					825					830				
Leu	Leu	Lys	Glu	Ala	Ile	His	Val	Ile	Ser	Cys	Gly	Tyr	Glu	Asp	Lys		
		835					840					845					
Thr	Asp	Trp	Gly	Lys	Glu	Ile	Gly	Trp	Ile	Tyr	Gly	Ser	Ile	Thr	Glu		
	850					855					860						
Asp	Ile	Leu	Thr	Gly	Phe	Lys	Met	His	Cys	His	Gly	Trp	Arg	Ser	Ile		
865					870					875					880		
Tyr	Cys	Ile	Pro	Lys	Arg	Pro	Ala	Phe	Lys	Gly	Ser	Ala	Pro	Leu	Asn		
				885					890					895			
Leu	Ser	Asp	Arg	Leu	His	Gln	Val	Leu	Arg	Trp	Ala	Leu	Gly	Ser	Val		
			900					905					910				
Glu	Ile	Phe	Phe	Ser	Lys	His	Cys	Pro	Leu	Trp	Tyr	Gly	Tyr	Gly	Gly		
		915					920					925					
Gly	Leu	Lys	Phe	Leu	Glu	Arg	Phe	Ser	Tyr	Ile	Asn	Ser	Ile	Val	Tyr		
	930					935					940						
Pro	Trp	Thr	Ser	Ile	Pro	Leu	Leu	Ala	Tyr	Cys	Thr	Leu	Pro	Ala	Ile		
945					950					955					960		
Cys	Leu	Leu	Thr	Gly	Lys	Phe	Ile	Thr	Pro	Glu	Leu	Thr	Asn	Val	Ala		
				965					970					975			
Ser	Ile	Trp	Phe	Met	Ala	Leu	Phe	Ile	Cys	Ile	Ser	Val	Thr	Gly	Ile		
			980					985					990				
Leu	Glu	Met	Arg	Trp	Ser	Gly	Val	Ala	Ile	Asp	Asp	Trp	Trp	Arg	Asn		
		995					1000					1005					
Glu	Gln	Phe	Trp	Val	Ile	Gly	Gly	Val	Ser	Ala	His	Leu	Phe	Ala	Val		
	1010					1015					1020						
Phe	Gln	Gly	Leu	Leu	Lys	Val	Phe	Ala	Gly	Ile	Asp	Thr	Ser	Phe	Thr		
1025					1030					1035					1040		
Val	Thr	Ser	Lys	Ala	Gly	Asp	Asp	Glu	Glu	Phe	Ser	Glu	Leu	Tyr	Thr		
				1045					1050					1055			
Phe	Lys	Trp	Thr	Thr	Leu	Leu	Ile	Pro	Pro	Thr	Thr	Leu	Leu	Leu	Leu		
			1060					1065					1070				

Asn Phe Ile Gly Val Val Ala Gly Ile Ser Asn Ala Ile Asn Asn Gly  
1075 1080 1085

Tyr Glu Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe Ala Phe Trp  
1090 1095 1100

Val Ile Val His Leu Tyr Pro Phe Leu Lys Gly Leu Val Gly Arg Gln  
1105 1110 1115 1120

Asn Arg Thr Pro Thr Ile Val Ile Val Trp Ser Ile Leu Leu Ala Ser  
1125 1130 1135

Ile Phe Ser Leu Leu Trp Val Arg Val Asp Pro Phe Leu Ala Lys Ser  
1140 1145 1150

Asn Gly Pro Leu Leu Glu Glu Cys Gly Leu Asp Cys Asn  
1155 1160 1165

<210> 9  
<211> 3936  
<212> DNA  
<213> Zea mays

<400> 9  
cttctccctc gtcggtgcgg cgtggcgcg ctcggcgcttc ggtgagaaac cactcggggg 60  
atgaggatct gctgctagag tgagaggagc tacggtcagt atcctctgcc ttcgtcggcg 120  
gcggaagtgg aggggaggaa gcgatggagg cgagcgccgg gctggtggcc ggctcccaca 180  
accgcaacga gctcgtcgtc atccgcccgc acggcgatcc cgggccgaag ccgcgcggg 240  
agcagaacgg gcaggtgtgc cagatttgcg gcgacgacgt cggccttgc cccggcggg 300  
accccttcgt ggcgtgcaac gagtgcgcct tccccgtctg ccgggactgc tacgaatacg 360  
agcgccggga gggcacgcag aactgcccc agtgcaagac tcgatacaag cgcctcaagg 420  
gctgccaaac tgtgaccggt gacgaggagg aggacggcgt cgatgacctg gacaacgagt 480  
tcaactggga cggccatgac tcgcagtctg tggccgagtc catgctctac ggccacatga 540  
gctacggccg tggaggtgac cctaattggc cgcacaagc ttccagctc aaccccaatg 600  
ttccactcct caccaacggg caaatggtg atgacatccc accggagcag cagcgctgg 660  
tgcttcttt catgggtggt gggggaaga ggatacatcc cttccttat gcggatccca 720  
gcttacctgt gcaacccagg tctatggacc catccaagga tcttgcgtca tatgggtatg 780  
gtagtggtgc ttggaaggaa cggatggaga attggaagca gagacaagag aggatgcacc 840  
agacggggaa tgatggtggt ggtgatgatg gtgacgatgc tgatctacca ctaatggatg 900  
aagcaagaca acaactgtcc aggaaaattc cacttccatc aagccagatt aatccatata 960  
ggatgattat cattattcgg cttgtggtt tggggttctt cttccactac cgagtgatgc 1020  
atccggtgaa tgcgtcattt gctttgtggc tcatatctgt tatctgtgaa atctggtttg 1080  
ccatgtcttg gattcttgat caattcccaa agtggttccc tattgagaga gagacttacc 1140  
tagaccggct gtcactgagg ttcgacaagg aaggccagcc atctcaactt gctccaattg 1200  
atctcttctg cagtacgggt gatcccttaa aggaacctcc tttggtcaca acaataactg 1260  
ttctatctat cctttcgggt gattatcctg ttgataaggt ttcttgctat gtttctgatg 1320  
atggtgctgc aatgctaacg tttgaagcat tatctgaaac atctgaattt gcaaagaaat 1380  
gggttccttt ctgcaaacgg tacaatattg aacctcgcg tccagagtgg tacttccaac 1440  
agaagataga ctacttgaaa gacaaggtgg cagcaaactt tgtagggag aggagagcaa 1500  
tgaagagaga gtatgaggaa ttcaaggtga gaatcaatgc cttagtgtgc aaagcccaga 1560  
aagttcctga agaaggatgg acaatgcaag atggaacccc ctggcctgga aacaatgttc 1620  
gtgatcatcc tggaatgatt caggtcttcc ttggccaaag cggaggcctt gactgtgagg 1680  
gaaatgaact gccacgattg gtttatgttt ctagagagaa acgaccaggc tataaccatc 1740  
ataagaaagc tgggtgctatg aatgcattgg tccgagtctc tgctgtacta acaaagtctc 1800  
catatttggt aaacttgat tgtgatcact acatacaaa cagcaaggct ataaaggaa 1860  
caatgtgttt tatgatggac cctttactag gaaagaaggt ttgctatgta cagttccctc 1920  
aaagatttga tgggattgat cgccatgacc gatatgctaa ccggaatgtt gtcttttttg 1980  
atatcaacat gaaaggtttg gatggtattc agggccaat ttatgttgt actggatgtg 2040  
tatttagaag gcaggcatta tatggttatg atgcccccaa aacaaagaag ccaccatcaa 2100  
ggacttgcaa ctgctggccc aagtgtgtct tttgctgttg ctgctttggc aataggaagc 2160

```

aaaagaagac taccaaacc aaaacagaga agaaaaagtt attatTTTTtC aagaaagaag 2220
agaaccaatc ccctgcatat gctcttggtg aaattgacga agctgctcca ggagctgaga 2280
atgaaaaggc cgggtattgta aatcaacaaa aattagaaaa gaaatttggc caatcttctg 2340
tttttggtac atccacactt ctcgagaatg gtggaacctt gaagagtgca agtcctgctt 2400
ctcttttgaa agaagctata catgtcatta gttgtgggta tgaagacaag acagactggg 2460
gaaaagagat tggctggatc tatggatcag ttacagaaga tattctaact ggtttcaaga 2520
tgcatgtgca tgggtggcgg tcaatttact gcatacctaa acgggttgca ttcaaagggt 2580
ctgcacctct gaatctttca gatcgtcttc accagggtgct tcgggtgggct cttgggtcta 2640
ttgagatctt cttcagcaat cattgcoctc tttgggtatgg gtatgggtggc ggtctgaaat 2700
ttttggaaag attttcctac atcaactcca tcgtgtatcc ttggacatct attccctct 2760
tggcttactg tacattgcct gccatctggt tattgacagg gaaatttatc actccagagc 2820
tgaataatgt tgccagcctg tgggttcatgt cactttttat ctgcattttt gctacgagca 2880
tcctagaaat gagatggagt ggtgttggaa ttgatgactg gtggaggaat gagcagttct 2940
gggtcattgg aggtgtgtcc tcacacctct ttgctgtgtt ccagggactt ctcaagggtca 3000
tagctggtgt tgatacaagc ttcaccgtga catcaaaggg tggagatgat gaggagttct 3060
cagagctata tacattcaaa tggactacct tattgatacc tcctaccacc ttgcttctat 3120
tgaacttcat tgggtgtggtc gctggcggtt caaatgcgat caataacgga tatgagtcac 3180
ggggcccccct ctttgggaag ctattctttg cattttgggt gattgtccat ctttatccct 3240
ttctcaaagg tttgggttga aggcaaaaaca ggacaccaac gattgtcatc gtctgggtcca 3300
ttctgctggc ttcaatcttc tcgctccttt gggttcggat tgatcctttc cttgcgaagg 3360
atgatgggtcc gcttcttgag gagtgtggtt tggattgcaa ctaggatgtc agtgcacag 3420
ctcccccaat ctgcatatgc ttgaagtata ttttctggtg tttgtcccca tattcagtgt 3480
ctgtagataa gagacatgaa atgtcccaag tttcttttga tccatggtga acctacttaa 3540
tatctgagag atatactggg ggaaaatgga ggctgcggca atccttgtgc agttgggccg 3600
tggaatacac catatgcaag tgtttgattt tgcagcattc tttattactt ggtcgcaata 3660
tagatgggct gagccgaaca gcaagggtatt ttgattctgc actgctcccg tgtacaaact 3720
tggttctcaa taaggcaggc aggaatgcat ctgccagtgg aacagagcaa cctgcacatt 3780
atztatgtat gcctgttcat tggagggtt gttcattaca tgttcgtcta tactagaaaa 3840
aacagaatat tagcattaat ctatagttaa ttaaagtatg taaatgcgcc tgttttttgt 3900
tgtgtactgt aatcatctga gttggttttg tgaaaa 3936

```

<210> 10  
 <211> 1086  
 <212> PRT  
 <213> Zea mays

<400> 10  
 Met Glu Ala Ser Ala Gly Leu Val Ala Gly Ser His Asn Arg Asn Glu  
 1 5 10 15  
 Leu Val Val Ile Arg Arg Asp Gly Asp Pro Gly Pro Lys Pro Pro Arg  
 20 25 30  
 Glu Gln Asn Gly Gln Val Cys Gln Ile Cys Gly Asp Asp Val Gly Leu  
 35 40 45  
 Ala Pro Gly Gly Asp Pro Phe Val Ala Cys Asn Glu Cys Ala Phe Pro  
 50 55 60  
 Val Cys Arg Asp Cys Tyr Glu Tyr Glu Arg Arg Glu Gly Thr Gln Asn  
 65 70 75 80  
 Cys Pro Gln Cys Lys Thr Arg Tyr Lys Arg Leu Lys Gly Cys Gln Arg  
 85 90 95  
 Val Thr Gly Asp Glu Glu Glu Asp Gly Val Asp Asp Leu Asp Asn Glu  
 100 105 110  
 Phe Asn Trp Asp Gly His Asp Ser Gln Ser Val Ala Glu Ser Met Leu  
 115 120 125

Tyr	Gly	His	Met	Ser	Tyr	Gly	Arg	Gly	Gly	Asp	Pro	Asn	Gly	Ala	Pro		
130						135					140						
Gln	Ala	Phe	Gln	Leu	Asn	Pro	Asn	Val	Pro	Leu	Leu	Thr	Asn	Gly	Gln		
145					150					155					160		
Met	Val	Asp	Asp	Ile	Pro	Pro	Glu	Gln	His	Ala	Leu	Val	Pro	Ser	Phe		
				165					170					175			
Met	Gly	Gly	Gly	Gly	Lys	Arg	Ile	His	Pro	Leu	Pro	Tyr	Ala	Asp	Pro		
			180					185					190				
Ser	Leu	Pro	Val	Gln	Pro	Arg	Ser	Met	Asp	Pro	Ser	Lys	Asp	Leu	Ala		
		195					200					205					
Ala	Tyr	Gly	Tyr	Gly	Ser	Val	Ala	Trp	Lys	Glu	Arg	Met	Glu	Asn	Trp		
210						215					220						
Lys	Gln	Arg	Gln	Glu	Arg	Met	His	Gln	Thr	Gly	Asn	Asp	Gly	Gly	Gly		
225					230					235					240		
Asp	Asp	Gly	Asp	Asp	Ala	Asp	Leu	Pro	Leu	Met	Asp	Glu	Ala	Arg	Gln		
				245					250					255			
Gln	Leu	Ser	Arg	Lys	Ile	Pro	Leu	Pro	Ser	Ser	Gln	Ile	Asn	Pro	Tyr		
			260					265					270				
Arg	Met	Ile	Ile	Ile	Ile	Arg	Leu	Val	Val	Leu	Gly	Phe	Phe	Phe	His		
		275					280					285					
Tyr	Arg	Val	Met	His	Pro	Val	Asn	Asp	Ala	Phe	Ala	Leu	Trp	Leu	Ile		
290						295					300						
Ser	Val	Ile	Cys	Glu	Ile	Trp	Phe	Ala	Met	Ser	Trp	Ile	Leu	Asp	Gln		
305					310					315					320		
Phe	Pro	Lys	Trp	Phe	Pro	Ile	Glu	Arg	Glu	Thr	Tyr	Leu	Asp	Arg	Leu		
				325					330					335			
Ser	Leu	Arg	Phe	Asp	Lys	Glu	Gly	Gln	Pro	Ser	Gln	Leu	Ala	Pro	Ile		
			340					345					350				
Asp	Phe	Phe	Val	Ser	Thr	Val	Asp	Pro	Leu	Lys	Glu	Pro	Pro	Leu	Val		
		355					360					365					
Thr	Thr	Asn	Thr	Val	Leu	Ser	Ile	Leu	Ser	Val	Asp	Tyr	Pro	Val	Asp		
370						375					380						
Lys	Val	Ser	Cys	Tyr	Val	Ser	Asp	Asp	Gly	Ala	Ala	Met	Leu	Thr	Phe		
385					390					395					400		
Glu	Ala	Leu	Ser	Glu	Thr	Ser	Glu	Phe	Ala	Lys	Lys	Trp	Val	Pro	Phe		
				405				410						415			
Cys	Lys	Arg	Tyr	Asn	Ile	Glu	Pro	Arg	Ala	Pro	Glu	Trp	Tyr	Phe	Gln		
			420					425					430				
Gln	Lys	Ile	Asp	Tyr	Leu	Lys	Asp	Lys	Val	Ala	Ala	Asn	Phe	Val	Arg		
		435					440					445					



Glu	Arg	Arg	Ala	Met	Lys	Arg	Glu	Tyr	Glu	Glu	Phe	Lys	Val	Arg	Ile
450						455					460				
Asn	Ala	Leu	Val	Ala	Lys	Ala	Gln	Lys	Val	Pro	Glu	Glu	Gly	Trp	Thr
465					470					475					480
Met	Gln	Asp	Gly	Thr	Pro	Trp	Pro	Gly	Asn	Asn	Val	Arg	Asp	His	Pro
				485					490					495	
Gly	Met	Ile	Gln	Val	Phe	Leu	Gly	Gln	Ser	Gly	Gly	Leu	Asp	Cys	Glu
			500					505					510		
Gly	Asn	Glu	Leu	Pro	Arg	Leu	Val	Tyr	Val	Ser	Arg	Glu	Lys	Arg	Pro
		515					520					525			
Gly	Tyr	Asn	His	His	Lys	Lys	Ala	Gly	Ala	Met	Asn	Ala	Leu	Val	Arg
	530					535					540				
Val	Ser	Ala	Val	Leu	Thr	Asn	Ala	Pro	Tyr	Leu	Leu	Asn	Leu	Asp	Cys
545					550					555					560
Asp	His	Tyr	Ile	Asn	Asn	Ser	Lys	Ala	Ile	Lys	Glu	Ala	Met	Cys	Phe
				565					570					575	
Met	Met	Asp	Pro	Leu	Leu	Gly	Lys	Lys	Val	Cys	Tyr	Val	Gln	Phe	Pro
			580					585					590		
Gln	Arg	Phe	Asp	Gly	Ile	Asp	Arg	His	Asp	Arg	Tyr	Ala	Asn	Arg	Asn
		595					600					605			
Val	Val	Phe	Phe	Asp	Ile	Asn	Met	Lys	Gly	Leu	Asp	Gly	Ile	Gln	Gly
	610					615					620				
Pro	Ile	Tyr	Val	Gly	Thr	Gly	Cys	Val	Phe	Arg	Arg	Gln	Ala	Leu	Tyr
625					630					635					640
Gly	Tyr	Asp	Ala	Pro	Lys	Thr	Lys	Lys	Pro	Pro	Ser	Arg	Thr	Cys	Asn
				645					650					655	
Cys	Trp	Pro	Lys	Trp	Cys	Phe	Cys	Cys	Cys	Cys	Phe	Gly	Asn	Arg	Lys
			660					665					670		
Gln	Lys	Lys	Thr	Thr	Lys	Pro	Lys	Thr	Glu	Lys	Lys	Lys	Leu	Leu	Phe
		675					680					685			
Phe	Lys	Lys	Glu	Glu	Asn	Gln	Ser	Pro	Ala	Tyr	Ala	Leu	Gly	Glu	Ile
	690					695					700				
Asp	Glu	Ala	Ala	Pro	Gly	Ala	Glu	Asn	Glu	Lys	Ala	Gly	Ile	Val	Asn
705					710					715					720
Gln	Gln	Lys	Leu	Glu	Lys	Lys	Phe	Gly	Gln	Ser	Ser	Val	Phe	Val	Thr
				725					730					735	
Ser	Thr	Leu	Leu	Glu	Asn	Gly	Gly	Thr	Leu	Lys	Ser	Ala	Ser	Pro	Ala
			740					745					750		
Ser	Leu	Leu	Lys	Glu	Ala	Ile	His	Val	Ile	Ser	Cys	Gly	Tyr	Glu	Asp
		755					760					765			

09900237.070601

Lys	Thr	Asp	Trp	Gly	Lys	Glu	Ile	Gly	Trp	Ile	Tyr	Gly	Ser	Val	Thr		
770						775					780						
Glu	Asp	Ile	Leu	Thr	Gly	Phe	Lys	Met	His	Cys	His	Gly	Trp	Arg	Ser		
785					790					795					800		
Ile	Tyr	Cys	Ile	Pro	Lys	Arg	Val	Ala	Phe	Lys	Gly	Ser	Ala	Pro	Leu		
				805					810					815			
Asn	Leu	Ser	Asp	Arg	Leu	His	Gln	Val	Leu	Arg	Trp	Ala	Leu	Gly	Ser		
			820					825					830				
Ile	Glu	Ile	Phe	Phe	Ser	Asn	His	Cys	Pro	Leu	Trp	Tyr	Gly	Tyr	Gly		
		835					840					845					
Gly	Gly	Leu	Lys	Phe	Leu	Glu	Arg	Phe	Ser	Tyr	Ile	Asn	Ser	Ile	Val		
	850					855					860						
Tyr	Pro	Trp	Thr	Ser	Ile	Pro	Leu	Leu	Ala	Tyr	Cys	Thr	Leu	Pro	Ala		
865					870					875					880		
Ile	Cys	Leu	Leu	Thr	Gly	Lys	Phe	Ile	Thr	Pro	Glu	Leu	Asn	Asn	Val		
				885					890					895			
Ala	Ser	Leu	Trp	Phe	Met	Ser	Leu	Phe	Ile	Cys	Ile	Phe	Ala	Thr	Ser		
			900					905					910				
Ile	Leu	Glu	Met	Arg	Trp	Ser	Gly	Val	Gly	Ile	Asp	Asp	Trp	Trp	Arg		
		915					920					925					
Asn	Glu	Gln	Phe	Trp	Val	Ile	Gly	Gly	Val	Ser	Ser	His	Leu	Phe	Ala		
	930					935					940						
Val	Phe	Gln	Gly	Leu	Leu	Lys	Val	Ile	Ala	Gly	Val	Asp	Thr	Ser	Phe		
945					950					955					960		
Thr	Val	Thr	Ser	Lys	Gly	Gly	Asp	Asp	Glu	Glu	Phe	Ser	Glu	Leu	Tyr		
				965					970					975			
Thr	Phe	Lys	Trp	Thr	Thr	Leu	Leu	Ile	Pro	Pro	Thr	Thr	Leu	Leu	Leu		
			980					985					990				
Leu	Asn	Phe	Ile	Gly	Val	Val	Ala	Gly	Val	Ser	Asn	Ala	Ile	Asn	Asn		
		995					1000					1005					
Gly	Tyr	Glu	Ser	Trp	Gly	Pro	Leu	Phe	Gly	Lys	Leu	Phe	Phe	Ala	Phe		
	1010					1015					1020						
Trp	Val	Ile	Val	His	Leu	Tyr	Pro	Phe	Leu	Lys	Gly	Leu	Val	Gly	Arg		
1025					1030					1035					1040		
Gln	Asn	Arg	Thr	Pro	Thr	Ile	Val	Ile	Val	Trp	Ser	Ile	Leu	Leu	Ala		
				1045					1050					1055			
Ser	Ile	Phe	Ser	Leu	Leu	Trp	Val	Arg	Ile	Asp	Pro	Phe	Leu	Ala	Lys		
			1060					1065					1070				
Asp	Asp	Gly	Pro	Leu	Leu	Glu	Glu	Cys	Gly	Leu	Asp	Cys	Asn				
	1075						1080					1085					

<210> 11  
 <211> 1138  
 <212> DNA  
 <213> Oryza sativa

<400> 11  
 cgctgctccc ggcgatggac gtgttcgtca ccaccgccga ccccgacaag gagccgccgc 60  
 tcgccacggc gaacaccgtg ctgtccatat atcctcgccg cgggctaccc cgccggcaag 120  
 gtgacgtgct atattttccga cgacgcaggc gcgagggtga cacgtaacgc ggtcgtggag 180  
 gcggccccgt tcgcggcgct ttgggtgtcg ttctgccgga agcacggcgt cgagccgagg 240  
 aacctggagg cgtacttcaa cgccggcgag ggtgggtggtg gcaaggcgaa ggtggtggcg 300  
 agggggagct acagggggat ggcgtggccg gagctggtgc gcgacaggag acgggtgcgc 360  
 cgcgagtacg aggagatgcg gctgcggtac gacgcgctgc aggccgccga tgcgcgccgc 420  
 cggcgccgcg gcgcggccga tgaccacgcc ggagttgtgc aggtactgat cgattttgct 480  
 gggagcgtgc cacagctcgg cgttgccaac gggagcaagc tcatcgacgt cgcctctgtc 540  
 gacgtgtgcc tcccggcgct tgtgtacgtg tgccgcgaga agcgcgcg cgacgcgcac 600  
 caccggaagg cgggcgccat gaacgcgcgc ttcatcctcg acctcgactg cgactactac 660  
 gtcaacaact cgcaggccct ccgcgcgcgc atctgcttca tgatcgaacg cggcggcggc 720  
 ggagccgccg aagacgcgcg cgcggtcgcg ttctgaccagt tcccgcagcg ggtcgacggc 780  
 gtcgatcccc gcgaccgcta cgccaaccac aaccgcgtcc tcttcgactg caccgagctc 840  
 ggctcgcagc gcctccaggg ccccatctac gtcggcaccg gctgcttgtt ccgccgtgtc 900  
 gcgctctaca gcgtcgacct gccgcgtgg agaccgcggc gttcattggg ctgtcgecta 960  
 ctcgagaag acgagcggct atggtccagg atgaaacaaa tggtaatatt aagtgttcca 1020  
 aggtgaaaaa ctcagctaaa acctgaccca agctgtaaca tgggtaaaaa tatatggccc 1080  
 aaaatgaaat ttactttttt ttttttacca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1138

<210> 12  
 <211> 341  
 <212> PRT  
 <213> Oryza sativa

<400> 12  
 Arg Cys Ser Arg Arg Trp Thr Cys Ser Ser Pro Pro Pro Thr Pro Thr  
 1 5 10 15  
 Arg Ser Arg Arg Ser Pro Arg Arg Thr Pro Cys Cys Pro Tyr Ile Leu  
 20 25 30  
 Ala Ala Gly Tyr Pro Ala Gly Lys Val Thr Cys Tyr Ile Ser Asp Asp  
 35 40 45  
 Ala Gly Ala Glu Val Thr Arg Asn Ala Val Val Glu Ala Ala Arg Phe  
 50 55 60  
 Ala Ala Leu Trp Val Ser Phe Cys Arg Lys His Gly Val Glu Pro Arg  
 65 70 75 80  
 Asn Leu Glu Ala Tyr Phe Asn Ala Gly Glu Gly Gly Gly Gly Lys Ala  
 85 90 95  
 Lys Val Val Ala Arg Gly Ser Tyr Arg Gly Met Ala Trp Pro Glu Leu  
 100 105 110  
 Val Arg Asp Arg Arg Arg Val Arg Arg Glu Tyr Glu Glu Met Arg Leu  
 115 120 125  
 Arg Ile Asp Ala Leu Gln Ala Ala Asp Ala Arg Arg Arg Arg Gly  
 130 135 140

Ala Ala Asp Asp His Ala Gly Val Val Gln Val Leu Ile Asp Phe Ala  
145 150 155 160

Gly Ser Val Pro Gln Leu Gly Val Ala Asn Gly Ser Lys Leu Ile Asp  
165 170 175

Val Ala Ser Val Asp Val Cys Leu Pro Ala Leu Val Tyr Val Cys Arg  
180 185 190

Glu Lys Arg Arg Gly His Ala His His Arg Lys Ala Gly Ala Met Asn  
195 200 205

Ala Pro Phe Ile Leu Asp Leu Asp Cys Asp Tyr Tyr Val Asn Asn Ser  
210 215 220

Gln Ala Leu Arg Ala Gly Ile Cys Phe Met Ile Glu Arg Gly Gly Gly  
225 230 235 240

Gly Ala Ala Glu Asp Ala Gly Ala Val Ala Phe Val Gln Phe Pro Gln  
245 250 255

Arg Val Asp Gly Val Asp Pro Gly Asp Arg Tyr Ala Asn His Asn Arg  
260 265 270

Val Leu Phe Asp Cys Thr Glu Leu Gly Leu Asp Gly Leu Gln Gly Pro  
275 280 285

Ile Tyr Val Gly Thr Gly Cys Leu Phe Arg Arg Val Ala Leu Tyr Ser  
290 295 300

Val Asp Leu Pro Arg Trp Arg Pro Arg Arg Ser Leu Gly Cys Arg Leu  
305 310 315 320

Leu Gly Glu Asp Glu Arg Leu Trp Ser Arg Met Lys Gln Met Val Ile  
325 330 335

Leu Ser Gly Pro Arg  
340

<210> 13  
<211> 3517  
<212> DNA  
<213> Glycine max

<400> 13  
gcacgagcca acaacaacac ccttatgtgg acacattagg tgagggttcaa cagctagcac 60  
caatcttcct tcataaaaca caaacctttg atcacacaat ctcaccttaa tttgtgttgt 120  
tgttgtgcca ttcccatatt gtcccattca ctaagacatg gaagccagcg ctggactggt 180  
cgctgggtca cataaccgca atgagctagt tgtcattcat ggccatgaag agccgaaggc 240  
tttgaagaac ttggatgggc aagtgtgtga gatttgtggt gatggcgtgg gactcacggt 300  
ggatggagac ttgtttgtgg cttgcaatga gtgtgtgttt ccagtgtgca ggccttgcta 360  
tgagtatgaa aggagagaag gaagccacct ttgcccacag tgcaaaaacca gatacaagcg 420  
tctcaaaggg agcccccgag tggagggaga tgatgatgaa gaggatgtgg atgatattga 480  
gcatgaattc aatattgatg agcaaaagaa caagcatggc cagggtgcag aagccatgct 540  
tcatgggagg atgagctatg gaagagggtcc tgaagatgat gacaattccc agttcccaac 600  
acctgtcatt gctgggtggtc gttctaggcc tgtaagtggg gagttcccaa tatcatctaa 660  
tgcttatggg gatcagatgt tctctcttc actgcataaa agagtgcac catatccagt 720  
gtctgaacct ggaagtgcaa gatgggacga aaaaaaaga agatggatgg aaagatagaa 780  
tggatgactg gaaattgcag caaggcaatt tggggcctga accggatgaa gatccagatg 840  
cagccatggt agatgaagca aggcaaccac tgtcaaggaa agtgccaata gcatccagca 900

```

aatcaatcc atatagaatg gtgattgtgg cacgtctggt tattcttgc tttctcctca 960
gatacagact catgaaccca gtacatgatg ccctggggct atggctaacc tctatcatat 1020
gtgaaatctg gtttgctttt tcatggattc tggatcagtt tcccaaattg tttccattg 1080
atagagagac ctaccttgac cgtctttcca tcaggatatga gcgtgaaggt gaaccaaaca 1140
tgcttgctcc tgtagatgtt tttgttagta ccgtggatcc catgaaggaa cctcctctgg 1200
ttacagcaaa cactgttctt tcaatcttgg ccatggatta cccggttgat aaaatatcat 1260
gctacatttc tgatgatgga gcctcaatgt gtacatttga gtccttatca gaaactgcag 1320
agtttgctag aaagtgggta ccgttttgta agaaattttc catagaacct cgggcacctg 1380
agatgtactt cagcgagaag attgactacc taaaggacaa agtgcaaccc acctttgtta 1440
aggagcgtcg agctatgaag aggggaatacg aagagtttaa ggtaggatac aatgcacttg 1500
ttgctaaggc ccagaaagtt cctcaggagag gatggatcat gcaggatggg acaccatggc 1560
caggaataaa cactaaggat catcctggta tgattcaagt gtttcttggg agcagtggag 1620
gtcttgatac tgaaggaaac caacttcctc gccttggtta tgtttccaga gagaaaaggc 1680
ctggttttca acaccacaag aaagctgggtg ccatgaatgc tctggttcgg gtatctgctg 1740
ttctcacaaa tgctcctttc atgttgaaat tggattgtga tcaactatgtc aataacagca 1800
aggctgcccg agaggccatg tgcttcttga tggaccacaa aactgggaag aaggtctgct 1860
atgtccagtt tcctcaaaga tttgatggta ttgatacaca tgatcgttat gccaacagga 1920
acacagtttt ctttgatatt aacatgaagg gtctagatgg tattcaaggc cctgtatatg 1980
tggggactgg atgtgttttc aggaggcaag ctttgatagg ctataatcct cccaagggtc 2040
caaagcgtcc aaaaatggtg agctgtgatt gtgtccgtg ttttggaagc cgaaaagtc 2100
ataaggagaa gaatgatgca aatggagagg ctgcaagcct aaaagggatg gatgatgaca 2160
aagaggtgtt gatgtcccaa atgaattttg agaagaaatt tggacaatcc tctatttttg 2220
tgacttctac cttgatggaa gaggtgtgtg tgctccttc ttcaagtcca gctgccctgc 2280
ttaaagaagc cattcatgtg attagctgtg gatatgaaga taaaactgaa tggggacttg 2340
agcttggttg gatctatgga tctatcacag aagatattct aacaggtttt aagatgcatt 2400
gccgtgggtg gaggtccatt tattgtatgc caaagagagc tgcattcaag ggtactgctc 2460
ctatcaactt gtcagatcgt ctcaaccagg ttcttcgttg ggcacttggg tccattgaga 2520
tttcttttag tcaccattgc cctcatggg atggcttcaa ggaaaagaag ctaaagtggc 2580
ttgagagatt tgcctatgca aacacaactg tctatccatt cacctccatt cctctagttg 2640
cctactgtat tcttcagca gtttgtttac tcaactgacaa attcatcatg ccaccgatta 2700
gcacctttgc tggtttgtac tttgttgctc tcttctcctc aatcattgca actgggtattc 2760
ttgagttgaa atggagtgga gtgagcattg aggaatgggt gagaaatgag cagttttggg 2820
tcattgggtg tgatcagct cacctctttg ctgttataca aggtctgcta aaggttctgg 2880
ctggaattga caccaatttc actgttacat caaaggcaac agatgatgaa gagtttggag 2940
aattgtacac ctttaagtgg actacactct tgattcctcc aaccactatt ttgatcatta 3000
acattgttgg tgtgttgct ggaatctcag atgccataaa caatgggtac caatcctggg 3060
gaccactctt tggaaagctc ttcttttctc tctgggtgat tgtccatctc tatccattcc 3120
ttaaagggtt gatgggtcgc caaaatcgca caccaccat tgttgtgatt tggtcagtgc 3180
tattggcctc tattttctcc ttactttggg taagaattga tccatttgct ctcaagacta 3240
agggacctga taccaagcta tgtggaatca actgctaaaa aagactgctt tccctatagt 3300
attattcttt aaaagatgta tgtagggtag atacattctt ggtttcacaa accaacaag 3360
tggcaatgca caagatcaa taaggaaaga gtgaaaattt tgtgtatcat aaatgagtgt 3420
tatcattttt gtaaatgttc tcaaggacat ctgttttggg tggaaactgcc caaaaattgc 3480
agttttatct attcactgga aaaaaaaaaa aaaaaaa 3517

```

<210> 14  
 <211> 1039  
 <212> PRT  
 <213> Glycine max

<220>  
 <221> UNSURE  
 <222> (201)

<400> 14  
 Met Glu Ala Ser Ala Gly Leu Val Ala Gly Ser His Asn Arg Asn Glu  
 1 5 10 15  
 Leu Val Val Ile His Gly His Glu Glu Pro Lys Ala Leu Lys Asn Leu  
 20 25 30

Asp Gly Gln Val Cys Glu Ile Cys Gly Asp Gly Val Gly Leu Thr Val  
 35 40 45  
 Asp Gly Asp Leu Phe Val Ala Cys Asn Glu Cys Gly Phe Pro Val Cys  
 50 55 60  
 Arg Pro Cys Tyr Glu Tyr Glu Arg Arg Glu Gly Ser His Leu Cys Pro  
 65 70 75 80  
 Gln Cys Lys Thr Arg Tyr Lys Arg Leu Lys Gly Ser Pro Arg Val Glu  
 85 90 95  
 Gly Asp Asp Asp Glu Glu Asp Val Asp Asp Ile Glu His Glu Phe Asn  
 100 105 110  
 Ile Asp Glu Gln Lys Asn Lys His Gly Gln Val Ala Glu Ala Met Leu  
 115 120 125  
 His Gly Arg Met Ser Tyr Gly Arg Gly Pro Glu Asp Asp Asp Asn Ser  
 130 135 140  
 Gln Phe Pro Thr Pro Val Ile Ala Gly Gly Arg Ser Arg Pro Val Ser  
 145 150 155 160  
 Gly Glu Phe Pro Ile Ser Ser Asn Ala Tyr Gly Asp Gln Met Leu Ser  
 165 170 175  
 Ser Ser Leu His Lys Arg Val His Pro Tyr Pro Val Ser Glu Pro Gly  
 180 185 190  
 Ser Ala Arg Trp Asp Glu Lys Lys Xaa Asp Gly Trp Lys Asp Arg Met  
 195 200 205  
 Asp Asp Trp Lys Leu Gln Gln Gly Asn Leu Gly Pro Glu Pro Asp Glu  
 210 215 220  
 Asp Pro Asp Ala Ala Met Leu Asp Glu Ala Arg Gln Pro Leu Ser Arg  
 225 230 235 240  
 Lys Val Pro Ile Ala Ser Ser Lys Ile Asn Pro Tyr Arg Met Val Ile  
 245 250 255  
 Val Ala Arg Leu Val Ile Leu Ala Phe Phe Leu Arg Tyr Arg Leu Met  
 260 265 270  
 Asn Pro Val His Asp Ala Leu Gly Leu Trp Leu Thr Ser Ile Ile Cys  
 275 280 285  
 Glu Ile Trp Phe Ala Phe Ser Trp Ile Leu Asp Gln Phe Pro Lys Trp  
 290 295 300  
 Phe Pro Ile Asp Arg Glu Thr Tyr Leu Asp Arg Leu Ser Ile Arg Tyr  
 305 310 315 320  
 Glu Arg Glu Gly Glu Pro Asn Met Leu Ala Pro Val Asp Val Phe Val  
 325 330 335  
 Ser Thr Val Asp Pro Met Lys Glu Pro Pro Leu Val Thr Ala Asn Thr  
 340 345 350

0900237.070601

Val	Leu	Ser	Ile	Leu	Ala	Met	Asp	Tyr	Pro	Val	Asp	Lys	Ile	Ser	Cys	355	360	365
Tyr	Ile	Ser	Asp	Asp	Gly	Ala	Ser	Met	Cys	Thr	Phe	Glu	Ser	Leu	Ser	370	375	380
Glu	Thr	Ala	Glu	Phe	Ala	Arg	Lys	Trp	Val	Pro	Phe	Cys	Lys	Lys	Phe	385	390	400
Ser	Ile	Glu	Pro	Arg	Ala	Pro	Glu	Met	Tyr	Phe	Ser	Glu	Lys	Ile	Asp	405	410	415
Tyr	Leu	Lys	Asp	Lys	Val	Gln	Pro	Thr	Phe	Val	Lys	Glu	Arg	Arg	Ala	420	425	430
Met	Lys	Arg	Glu	Tyr	Glu	Glu	Phe	Lys	Val	Arg	Ile	Asn	Ala	Leu	Val	435	440	445
Ala	Lys	Ala	Gln	Lys	Val	Pro	Gln	Gly	Gly	Trp	Ile	Met	Gln	Asp	Gly	450	455	460
Thr	Pro	Trp	Pro	Gly	Asn	Asn	Thr	Lys	Asp	His	Pro	Gly	Met	Ile	Gln	465	470	475
Val	Phe	Leu	Gly	Ser	Ser	Gly	Gly	Leu	Asp	Thr	Glu	Gly	Asn	Gln	Leu	485	490	495
Pro	Arg	Leu	Val	Tyr	Val	Ser	Arg	Glu	Lys	Arg	Pro	Gly	Phe	Gln	His	500	505	510
His	Lys	Lys	Ala	Gly	Ala	Met	Asn	Ala	Leu	Val	Arg	Val	Ser	Ala	Val	515	520	525
Leu	Thr	Asn	Ala	Pro	Phe	Met	Leu	Asn	Leu	Asp	Cys	Asp	His	Tyr	Val	530	535	540
Asn	Asn	Ser	Lys	Ala	Ala	Arg	Glu	Ala	Met	Cys	Phe	Leu	Met	Asp	Pro	545	550	555
Gln	Thr	Gly	Lys	Lys	Val	Cys	Tyr	Val	Gln	Phe	Pro	Gln	Arg	Phe	Asp	565	570	575
Gly	Ile	Asp	Thr	His	Asp	Arg	Tyr	Ala	Asn	Arg	Asn	Thr	Val	Phe	Phe	580	585	590
Asp	Ile	Asn	Met	Lys	Gly	Leu	Asp	Gly	Ile	Gln	Gly	Pro	Val	Tyr	Val	595	600	605
Gly	Thr	Gly	Cys	Val	Phe	Arg	Arg	Gln	Ala	Leu	Tyr	Gly	Tyr	Asn	Pro	610	615	620
Pro	Lys	Gly	Pro	Lys	Arg	Pro	Lys	Met	Val	Ser	Cys	Asp	Cys	Cys	Pro	625	630	635
Cys	Phe	Gly	Ser	Arg	Lys	Lys	Tyr	Lys	Glu	Lys	Asn	Asp	Ala	Asn	Gly	645	650	655
Glu	Ala	Ala	Ser	Leu	Lys	Gly	Met	Asp	Asp	Asp	Lys	Glu	Val	Leu	Met	660	665	670

Ser	Gln	Met	Asn	Phe	Glu	Lys	Lys	Phe	Gly	Gln	Ser	Ser	Ile	Phe	Val
		675					680					685			
Thr	Ser	Thr	Leu	Met	Glu	Glu	Gly	Gly	Val	Pro	Pro	Ser	Ser	Ser	Pro
	690					695					700				
Ala	Ala	Leu	Leu	Lys	Glu	Ala	Ile	His	Val	Ile	Ser	Cys	Gly	Tyr	Glu
705					710					715					720
Asp	Lys	Thr	Glu	Trp	Gly	Leu	Glu	Leu	Gly	Trp	Ile	Tyr	Gly	Ser	Ile
				725					730					735	
Thr	Glu	Asp	Ile	Leu	Thr	Gly	Phe	Lys	Met	His	Cys	Arg	Gly	Trp	Arg
			740					745					750		
Ser	Ile	Tyr	Cys	Met	Pro	Lys	Arg	Ala	Ala	Phe	Lys	Gly	Thr	Ala	Pro
		755					760					765			
Ile	Asn	Leu	Ser	Asp	Arg	Leu	Asn	Gln	Val	Leu	Arg	Trp	Ala	Leu	Gly
	770					775					780				
Ser	Ile	Glu	Ile	Phe	Phe	Ser	His	His	Cys	Pro	Leu	Trp	Tyr	Gly	Phe
785					790					795					800
Lys	Glu	Lys	Lys	Leu	Lys	Trp	Leu	Glu	Arg	Phe	Ala	Tyr	Ala	Asn	Thr
				805					810					815	
Thr	Val	Tyr	Pro	Phe	Thr	Ser	Ile	Pro	Leu	Val	Ala	Tyr	Cys	Ile	Leu
			820					825					830		
Pro	Ala	Val	Cys	Leu	Leu	Thr	Asp	Lys	Phe	Ile	Met	Pro	Pro	Ile	Ser
		835					840					845			
Thr	Phe	Ala	Gly	Leu	Tyr	Phe	Val	Ala	Leu	Phe	Ser	Ser	Ile	Ile	Ala
	850					855					860				
Thr	Gly	Ile	Leu	Glu	Leu	Lys	Trp	Ser	Gly	Val	Ser	Ile	Glu	Glu	Trp
865					870					875					880
Trp	Arg	Asn	Glu	Gln	Phe	Trp	Val	Ile	Gly	Gly	Val	Ser	Ala	His	Leu
				885					890					895	
Phe	Ala	Val	Ile	Gln	Gly	Leu	Leu	Lys	Val	Leu	Ala	Gly	Ile	Asp	Thr
			900					905					910		
Asn	Phe	Thr	Val	Thr	Ser	Lys	Ala	Thr	Asp	Asp	Glu	Glu	Phe	Gly	Glu
		915					920					925			
Leu	Tyr	Thr	Phe	Lys	Trp	Thr	Thr	Leu	Leu	Ile	Pro	Pro	Thr	Thr	Ile
	930					935					940				
Leu	Ile	Ile	Asn	Ile	Val	Gly	Val	Val	Ala	Gly	Ile	Ser	Asp	Ala	Ile
945					950					955					960
Asn	Asn	Gly	Tyr	Gln	Ser	Trp	Gly	Pro	Leu	Phe	Gly	Lys	Leu	Phe	Phe
				965					970					975	
Ser	Phe	Trp	Val	Ile	Val	His	Leu	Tyr	Pro	Phe	Leu	Lys	Gly	Leu	Met
			980					985					990		



Gly Arg Gln Asn Arg Thr Pro Thr Ile Val Val Ile Trp Ser Val Leu  
 995 1000 1005

Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Arg Ile Asp Pro Phe Val  
 1010 1015 1020

Leu Lys Thr Lys Gly Pro Asp Thr Lys Leu Cys Gly Ile Asn Cys  
 1025 1030 1035

<210> 15  
 <211> 2125  
 <212> DNA  
 <213> Glycine max

<400> 15  
 gccaaagctc agaagatgcc agaggaaggt tggacaatgc aggatggaac tccttggcct 60  
 ggaaataatc ctagggatca tccgggaatg attcaggtgt ttttaggtca tagtgggggg 120  
 ctggatacag atggaaatga gctgcctaga cttgtttatg tttctcgtga gaagcgacca 180  
 ggcttccaac atcacaagaa ggctggagct atgaatgctt tgattcgagt ttctgctgtc 240  
 ttgaccaatg gtgcataatc tctgaatgtg gattgtgatc actatttcaa taatagcaaa 300  
 gccctcaaaag aagccatgtg tttcatgatg gatcctgttc ttggaaagaa gacatgctat 360  
 gttcaatttc ctcagagatt tgacggcatt gacttgcacg atcgatatgc caatcgcaat 420  
 attgtgttct ttgatatcaa catgaaaggt caggatgggtg ttcaggggccc agtctatgtg 480  
 ggaactgggtt gttgtttcaa taggcaagct ttgtatgggt atgatcctgt tttgactgag 540  
 gaagatttgg aacctaacat tattgtaaag agttgttgcg gttctagaaa gaagggaaaag 600  
 ggtggcaata agaagtacag tgacaagaag aaggcgatgg gaagaactga atccactgta 660  
 cccatattta atatggaaga catagaggag ggtgttgaag gttatgatga tgaaaggaca 720  
 ctacttatgt ctcaaaagag cttggagaag cgttttggtc agtctccagt ttttattgct 780  
 gccactttca tggagcaggg tggcattcca ccttcaacga accctgcaac tcttcttaag 840  
 gaagcaatcc atgttatcag ctgtggttac gaagacaaga cagaatgggg caaagagatt 900  
 ggtatgatct atggtctctg gacagaagat atccttgactg ggttcaagat gcatgctcgt 960  
 gggttgattt ccatctattg catgccacct cgccagcat ttaagggttc tgctcctatc 1020  
 aatctttctg atcgtctcaa tcaggtgctt cgggtggcct tgggttcaat tgagatcttt 1080  
 ctaagcaggc attgtccctt gtggtatggc tacaatggga agttgaagcc tctgatgagg 1140  
 cttgcttata ttaacaccat tgtctacccg tttacctcaa tccattgat tgcttactgt 1200  
 acgcttcctg catttttgtct tctcacaat aaattttatta ttcctgagat aagcaacttt 1260  
 gccagtatgt ggttcattct tctctttgtc tccattttta ccacttcaat tcttgagctt 1320  
 aggtggagtg gggtcagtat agaagactgg tggagaaatg aacagttctg gggtatcggg 1380  
 gggacatctg cgcactctct tgctgtgttc caggggcttc taaaagtgtc tgctgggagc 1440  
 gatacaaaatt ttactgttac atcgaaggca tcggacgagg atggggactt tgccgagctt 1500  
 tatgtgttta aatggacatc acttctcatc cctcctacaa cagtgtctat tgtgaatttg 1560  
 gttgggattg tggctggtgt atcctatgcc ataaacagtg gttaccagtc ttgggggtcca 1620  
 ctatttggca agctgttctt tgctatctgg gtcattgccc atctataccc attcttgaag 1680  
 ggtctcttgg gcaggcaaaa tcgtacccca accattgtta ttgtttgggt cgttcttctt 1740  
 gcttcaatat tctccttgcg gtgggtgagg attgatccct tcacctctga ctccaacaaa 1800  
 ttaaccaatg gtcaatgtgg catcaactgt tagttctctt gtatgattca ttttgtgttg 1860  
 ttattccctt ttgcttggag atacacaagg ttgctgtcgt gtatatagca agaattttca 1920  
 gcctatcaaa gttgtctgga ggattgaacc cctgaaatag atgggaatgt accctctctg 1980  
 tttctattat ttatctacat gttccttaca agaatagtca gtagtaatgt tgaggtgtat 2040  
 gttatatattt tccccacag aatataaatt tgttcatgcy aatatttaat gaaagccaac 2100  
 aaggctcctg gttgttttgt tcttt 2125

<210> 16  
 <211> 610  
 <212> PRT  
 <213> Glycine max

09900237.070601

```

<400> 16
Ala Lys Ala Gln Lys Met Pro Glu Glu Gly Trp Thr Met Gln Asp Gly
 1          5          10          15

Thr Pro Trp Pro Gly Asn Asn Pro Arg Asp His Pro Gly Met Ile Gln
          20          25          30

Val Phe Leu Gly His Ser Gly Gly Leu Asp Thr Asp Gly Asn Glu Leu
          35          40          45

Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Phe Gln His
          50          55          60

His Lys Lys Ala Gly Ala Met Asn Ala Leu Ile Arg Val Ser Ala Val
 65          70          75          80

Leu Thr Asn Gly Ala Tyr Leu Leu Asn Val Asp Cys Asp His Tyr Phe
          85          90          95

Asn Asn Ser Lys Ala Leu Lys Glu Ala Met Cys Phe Met Met Asp Pro
          100          105          110

Val Leu Gly Lys Lys Thr Cys Tyr Val Gln Phe Pro Gln Arg Phe Asp
          115          120          125

Gly Ile Asp Leu His Asp Arg Tyr Ala Asn Arg Asn Ile Val Phe Phe
          130          135          140

Asp Ile Asn Met Lys Gly Gln Asp Gly Val Gln Gly Pro Val Tyr Val
          145          150          155          160

Gly Thr Gly Cys Cys Phe Asn Arg Gln Ala Leu Tyr Gly Tyr Asp Pro
          165          170          175

Val Leu Thr Glu Glu Asp Leu Glu Pro Asn Ile Ile Val Lys Ser Cys
          180          185          190

Cys Gly Ser Arg Lys Lys Gly Lys Gly Gly Asn Lys Lys Tyr Ser Asp
          195          200          205

Lys Lys Lys Ala Met Gly Arg Thr Glu Ser Thr Val Pro Ile Phe Asn
          210          215          220

Met Glu Asp Ile Glu Glu Gly Val Glu Gly Tyr Asp Asp Glu Arg Thr
          225          230          235          240

Leu Leu Met Ser Gln Lys Ser Leu Glu Lys Arg Phe Gly Gln Ser Pro
          245          250          255

Val Phe Ile Ala Ala Thr Phe Met Glu Gln Gly Gly Ile Pro Pro Ser
          260          265          270

Thr Asn Pro Ala Thr Leu Leu Lys Glu Ala Ile His Val Ile Ser Cys
          275          280          285

Gly Tyr Glu Asp Lys Thr Glu Trp Gly Lys Glu Ile Gly Trp Ile Tyr
          290          295          300

Gly Ser Val Thr Glu Asp Ile Leu Thr Gly Phe Lys Met His Ala Arg
          305          310          315          320

```

Gly Trp Ile Ser Ile Tyr Cys Met Pro Pro Arg Pro Ala Phe Lys Gly  
325 330 335

Ser Ala Pro Ile Asn Leu Ser Asp Arg Leu Asn Gln Val Leu Arg Trp  
340 345 350

Ala Leu Gly Ser Ile Glu Ile Phe Leu Ser Arg His Cys Pro Leu Trp  
355 360 365

Tyr Gly Tyr Asn Gly Lys Leu Lys Pro Leu Met Arg Leu Ala Tyr Ile  
370 375 380

Asn Thr Ile Val Tyr Pro Phe Thr Ser Ile Pro Leu Ile Ala Tyr Cys  
385 390 395 400

Thr Leu Pro Ala Phe Cys Leu Leu Thr Asn Lys Phe Ile Ile Pro Glu  
405 410 415

Ile Ser Asn Phe Ala Ser Met Trp Phe Ile Leu Leu Phe Val Ser Ile  
420 425 430

Phe Thr Thr Ser Ile Leu Glu Leu Arg Trp Ser Gly Val Ser Ile Glu  
435 440 445

Asp Trp Trp Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Thr Ser Ala  
450 455 460

His Leu Phe Ala Val Phe Gln Gly Leu Leu Lys Val Leu Ala Gly Ile  
465 470 475 480

Asp Thr Asn Phe Thr Val Thr Ser Lys Ala Ser Asp Glu Asp Gly Asp  
485 490 495

Phe Ala Glu Leu Tyr Val Phe Lys Trp Thr Ser Leu Leu Ile Pro Pro  
500 505 510

Thr Thr Val Leu Ile Val Asn Leu Val Gly Ile Val Ala Gly Val Ser  
515 520 525

Tyr Ala Ile Asn Ser Gly Tyr Gln Ser Trp Gly Pro Leu Phe Gly Lys  
530 535 540

Leu Phe Phe Ala Ile Trp Val Ile Ala His Leu Tyr Pro Phe Leu Lys  
545 550 555 560

Gly Leu Leu Gly Arg Gln Asn Arg Thr Pro Thr Ile Val Ile Val Trp  
565 570 575

Ser Val Leu Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Arg Ile Asp  
580 585 590

Pro Phe Thr Ser Asp Ser Asn Lys Leu Thr Asn Gly Gln Cys Gly Ile  
595 600 605

Asn Cys  
610

<210> 17  
<211> 2890

<212> DNA  
 <213> Glycine max

<400> 17

```
gcacgagctc caccaggtta atgatgcata tggcttgtgg ttgacatcag tcatctgtga 60
aatatggttt gctgtatcat ggataatgga tcagtttcca aaatggtacc caatacagcg 120
agaaacatac cttgatcgtc tgtcactcag gtatgaaaaa gaagggaagc catctgagtt 180
gtccagtgtg gacgtctttg tcagtactgt tgatcccatg aaggaaacct cactgattac 240
agcaaacact gttctatcta tccttgctgt tgattatcca gttgataaag ttgcatgcta 300
tgtctcagat gatggtgctg ctatgcttac ttttgaagca ctgtctgaga catctgaatt 360
tgctaggaga tgggttccat tttgtaagaa atacaatatt gagccccggg caccagaatg 420
gtacttttgt cagaagatgg actatctgaa aaataaagta caccagcat ttgtcaggga 480
aaggagagca atgaagaggg attatgaaga atttaagggt aggattaaca gtttggtggc 540
aacagcacia aaggttcctg aggatggatg gaccatgcaa gatgggactc cttggcctgg 600
aaataatgtg agggatcatc ctggcatgat tcaggtcttc cttgggcagg atggtgttcg 660
tgatgttgaa ggaaatgagc taccocgctt ggtctacgtt tctagagaaa agaggccagg 720
gtttgatcac caaaaaagg ctggtgcaat gaatgctctg gtacgggctt cagcaattat 780
cactaatgca ccctatcttc tgaatgttga ttgtgatcac tacattaaca atagcaaggc 840
acttagagaa gctatgtgtt ttatgatgga tcctcaacta gggaaaaagg tttgctatgt 900
gcaatttctc cagcgatttg atggaattga tagacatgat agatattcaa acagaaatgt 960
tgtatttttc gatattaaca tgaaaggatt ggatgggata caagggtcca tatatgtcgg 1020
aactggatgt gttttcagaa ggtacgcact ttatggatat gatgcacctg ccaagaagaa 1080
accaccgagc aaaacttgta actggtggcc aaagtgggtg tgccatgttt gtggctctag 1140
aaagaaaaag aatgccataa gtaagaagga gaaaaagagg aaggtgaagc acagtgaagc 1200
atcaaagcag atacatgcac ttgaaaatat tgaggcgggg aatgaaggaa ccaacaatga 1260
gaagacatcc aatctgactc aaacaaagtt ggagaagagg tttggacagt ctccagtatt 1320
tgtagcctcc acacttttgg atgatggtgg agttccacat ggcgtgagtc ctgcatcact 1380
tttaaaagaa gccatccagg tcatcagttg tggttatgaa gacaaaacag aatgggggaa 1440
agaagttggg tggatatatg gttctgtgac agaggatatc ttgactggat ttaaaatgca 1500
ttgccatggt tggcggtctg tgtattgcat tcctaagcgg cctgcattta aggggtctgc 1560
gcctatcaac ctttcagatc gtctgcacca agttcttcgg tgggctcttg ggtctgttga 1620
gatttttttc agcagacatt gtccaatctg gtatggctat ggtggtggat tgaaattgtt 1680
ggaacgattt tctacatta actcggctcg atatccctgg acttccctcc cattgcttgt 1740
ctactgtact ctaccagcca tatgccttct gacttgaaaa ttatcgtac ccgagattag 1800
caactatgcc agtcttgtgt tcatggccct ctcatatcc attgcagcaa ctggcatcct 1860
tgagatgcaa tggggcggtg ttagcataga cgactggtgg aggaacgaac agttttgggt 1920
gatcgagggt gtttcttccc atctatttgc cctatttcag ggtttactga aggtcttggc 1980
tgggtgtgaa acaaacttca ctgtgacctc aaaagcagca gatgatggag aattctcaga 2040
actctacata ttcaagtgga catcactctt gatccctcca atgactttac ttatcatgaa 2100
tattgtcggg gtggttgtcg ggatctcaga tgccatcaac aatggttatg actcatgggg 2160
acctctcttt ggtagattgt tctttgcatt gtgggtgatc ctccatctct accccttctt 2220
gaagggggtt cttggaaaac aagatagaat gccaacatt atattggttt ggtcaatcct 2280
tctggcctcc atcttgactc tcatgtgggt cagaattaac ccgtttgtgt caagagacgg 2340
ccccgtgtta gaaatttgtg gattgaattg cgacgagtcg tgaataaaga aaagctgaag 2400
aagaagggtt agttattttt cagctacact gcagtcatgt tgaagaatgc agccagcaca 2460
tgcttcacaa agttgcacga attttcggat ggaagtttta ttttccgggt gtgtagagat 2520
taaagagagg aaggggaggg ggctgacaca ttgttacctt gtaatagggt tttttcattt 2580
attctttgat tatattttct gtgggtttta gtgttattct ctttccagtt tcatgtatta 2640
taagaaagag gcattgaatg ataaattatt ccctcttcaa aatgggggat cctcagctc 2700
aagaaattac ttggtcatat ttttaggtat gggcttgtgt ctgtttaaaa ccatttgtaa 2760
taccgtcaaa actatggata ttcttgttcc tcagatgtgt ttttgtgttt tattatttaa 2820
cactcaggaa ccttttgggt tgattcaatt attcaatgtt tggatggcac taaaaaaaaa 2880
aaaaaaaaaa 2890
```

<210> 18  
 <211> 793  
 <212> PRT  
 <213> Glycine max

```

<400> 18
His Glu Leu His Pro Val Asn Asp Ala Tyr Gly Leu Trp Leu Thr Ser
 1          5          10          15

Val Ile Cys Glu Ile Trp Phe Ala Val Ser Trp Ile Met Asp Gln Phe
          20          25          30

Pro Lys Trp Tyr Pro Ile Gln Arg Glu Thr Tyr Leu Asp Arg Leu Ser
          35          40          45

Leu Arg Tyr Glu Lys Glu Gly Lys Pro Ser Glu Leu Ser Ser Val Asp
 50          55          60

Val Phe Val Ser Thr Val Asp Pro Met Lys Glu Pro Pro Leu Ile Thr
 65          70          75          80

Ala Asn Thr Val Leu Ser Ile Leu Ala Val Asp Tyr Pro Val Asp Lys
          85          90          95

Val Ala Cys Tyr Val Ser Asp Asp Gly Ala Ala Met Leu Thr Phe Glu
          100          105          110

Ala Leu Ser Glu Thr Ser Glu Phe Ala Arg Arg Trp Val Pro Phe Cys
          115          120          125

Lys Lys Tyr Asn Ile Glu Pro Arg Ala Pro Glu Trp Tyr Phe Gly Gln
          130          135          140

Lys Met Asp Tyr Leu Lys Asn Lys Val His Pro Ala Phe Val Arg Glu
          145          150          155          160

Arg Arg Ala Met Lys Arg Asp Tyr Glu Glu Phe Lys Val Arg Ile Asn
          165          170          175

Ser Leu Val Ala Thr Ala Gln Lys Val Pro Glu Asp Gly Trp Thr Met
          180          185          190

Gln Asp Gly Thr Pro Trp Pro Gly Asn Asn Val Arg Asp His Pro Gly
          195          200          205

Met Ile Gln Val Phe Leu Gly Gln Asp Gly Val Arg Asp Val Glu Gly
          210          215          220

Asn Glu Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly
          225          230          235          240

Phe Asp His His Lys Lys Ala Gly Ala Met Asn Ala Leu Val Arg Ala
          245          250          255

Ser Ala Ile Ile Thr Asn Ala Pro Tyr Leu Leu Asn Val Asp Cys Asp
          260          265          270

His Tyr Ile Asn Asn Ser Lys Ala Leu Arg Glu Ala Met Cys Phe Met
          275          280          285

Met Asp Pro Gln Leu Gly Lys Lys Val Cys Tyr Val Gln Phe Pro Gln
          290          295          300

Arg Phe Asp Gly Ile Asp Arg His Asp Arg Tyr Ser Asn Arg Asn Val
          305          310          315          320

```

Val	Phe	Phe	Asp	Ile	Asn	Met	Lys	Gly	Leu	Asp	Gly	Ile	Gln	Gly	Pro	
				325					330					335		
Ile	Tyr	Val	Gly	Thr	Gly	Cys	Val	Phe	Arg	Arg	Tyr	Ala	Leu	Tyr	Gly	
			340					345					350			
Tyr	Asp	Ala	Pro	Ala	Lys	Lys	Lys	Pro	Pro	Ser	Lys	Thr	Cys	Asn	Cys	
		355					360					365				
Trp	Pro	Lys	Trp	Cys	Cys	Leu	Cys	Cys	Gly	Ser	Arg	Lys	Lys	Lys	Asn	
	370					375					380					
Ala	Asn	Ser	Lys	Lys	Glu	Lys	Lys	Arg	Lys	Val	Lys	His	Ser	Glu	Ala	
385					390					395					400	
Ser	Lys	Gln	Ile	His	Ala	Leu	Glu	Asn	Ile	Glu	Ala	Gly	Asn	Glu	Gly	
				405					410					415		
Thr	Asn	Asn	Glu	Lys	Thr	Ser	Asn	Leu	Thr	Gln	Thr	Lys	Leu	Glu	Lys	
			420					425					430			
Arg	Phe	Gly	Gln	Ser	Pro	Val	Phe	Val	Ala	Ser	Thr	Leu	Leu	Asp	Asp	
		435					440					445				
Gly	Gly	Val	Pro	His	Gly	Val	Ser	Pro	Ala	Ser	Leu	Leu	Lys	Glu	Ala	
	450					455					460					
Ile	Gln	Val	Ile	Ser	Cys	Gly	Tyr	Glu	Asp	Lys	Thr	Glu	Trp	Gly	Lys	
465					470					475					480	
Glu	Val	Gly	Trp	Ile	Tyr	Gly	Ser	Val	Thr	Glu	Asp	Ile	Leu	Thr	Gly	
				485					490					495		
Phe	Lys	Met	His	Cys	His	Gly	Trp	Arg	Ser	Val	Tyr	Cys	Ile	Pro	Lys	
			500					505					510			
Arg	Pro	Ala	Phe	Lys	Gly	Ser	Ala	Pro	Ile	Asn	Leu	Ser	Asp	Arg	Leu	
		515					520					525				
His	Gln	Val	Leu	Arg	Trp	Ala	Leu	Gly	Ser	Val	Glu	Ile	Phe	Phe	Ser	
	530					535					540					
Arg	His	Cys	Pro	Ile	Trp	Tyr	Gly	Tyr	Gly	Gly	Gly	Leu	Lys	Leu	Leu	
545					550					555					560	
Glu	Arg	Phe	Ser	Tyr	Ile	Asn	Ser	Val	Val	Tyr	Pro	Trp	Thr	Ser	Leu	
				565					570					575		
Pro	Leu	Leu	Val	Tyr	Cys	Thr	Leu	Pro	Ala	Ile	Cys	Leu	Leu	Thr	Gly	
			580					585					590			
Lys	Phe	Ile	Val	Pro	Glu	Ile	Ser	Asn	Tyr	Ala	Ser	Leu	Val	Phe	Met	
		595					600					605				
Ala	Leu	Phe	Ile	Ser	Ile	Ala	Ala	Thr	Gly	Ile	Leu	Glu	Met	Gln	Trp	
	610					615					620					
Gly	Gly	Val	Ser	Ile	Asp	Asp	Trp	Trp	Arg	Asn	Glu	Gln	Phe	Trp	Val	
625					630					635					640	

Ile Gly Gly Val Ser Ser His Leu Phe Ala Leu Phe Gln Gly Leu Leu  
645 650 655

Lys Val Leu Ala Gly Val Asn Thr Asn Phe Thr Val Thr Ser Lys Ala  
660 665 670

Ala Asp Asp Gly Glu Phe Ser Glu Leu Tyr Ile Phe Lys Trp Thr Ser  
675 680 685

Leu Leu Ile Pro Pro Met Thr Leu Leu Ile Met Asn Ile Val Gly Val  
690 695 700

Val Val Gly Ile Ser Asp Ala Ile Asn Asn Gly Tyr Asp Ser Trp Gly  
705 710 715 720

Pro Leu Phe Gly Arg Leu Phe Phe Ala Leu Trp Val Ile Leu His Leu  
725 730 735

Tyr Pro Phe Leu Lys Gly Leu Leu Gly Lys Gln Asp Arg Met Pro Thr  
740 745 750

Ile Ile Leu Val Trp Ser Ile Leu Leu Ala Ser Ile Leu Thr Leu Met  
755 760 765

Trp Val Arg Ile Asn Pro Phe Val Ser Arg Asp Gly Pro Val Leu Glu  
770 775 780

Ile Cys Gly Leu Asn Cys Asp Glu Ser  
785 790

<210> 19  
<211> 1733  
<212> DNA  
<213> Triticum aestivum

<220>  
<221> unsure  
<222> (262)

<400> 19  
gaagctatgt gcttctaat ggatccaaac ctaggtccgc aagtctgtta tgtgcagttc 60  
ccacaaaggt ttgatggtat tgataggaat gatcgatatg caaacaggaa cactgtcttt 120  
tttgatatta acttgagggg ccttgacggc attcaaggac cagtttatgt gggaactggg 180  
tgtgttttca acagaacggc tatctatggg tatgagcccc caattaaggc gaagaagcca 240  
ggtttcttgg catcattatg tnggggcaag aagaaggcaa gcaagtcaaa gaaaaggagc 300  
tcagataaga aaaagtcgaa caagcatgtg gacagttctg ttccagtatt caatctcgaa 360  
gacatagagg aggggtgtga aggtgctggg ttgatgatg agaaatcagt tctcatgtct 420  
caaatgagct tagagaagag atttggccag tcagcagcat ttgttgccct cactctgatg 480  
gaatatggtg gtgttcctca gtcgtccact ccagaatctc ttttgaaaga agctatccat 540  
gtcataagtt gtggctatga ggacaagtct gaatggggaa ctgagattgg ttggatctat 600  
ggatctgtca cagaagatat tctaactgga ttcaagatgc acgcaagagg ctggcggttca 660  
atctattgca tgcccaagcg cccagcttct aagggatctg ccccatcaa tctttcagat 720  
cgtctgaatc aagtgtgtcg gtgggtctct ggttctgttg aaattctttt cagccggcat 780  
tgccccttat ggtatggcta cggaggggcg ctcaagttcc tggagagatt cgcttacatc 840  
aacaccacca tttaccact aacctctctc ccgcttctag tctattgtat attgcctgct 900  
atctgtctgc tcactggaaa gttcatcatg ccagagatta gcaacttggc cagtatctgg 960  
ttcattgctg tcttcctttc aattttcgcc actggtatcc ttgagatgag gtggagtggg 1020  
gttggcattg acgagtgggt gaggaatgaa cagttctggg tcattggagg tatctctgcc 1080

```

catctgtttg ccgctctttca gggctcttctg aaggtgcttg caggtatcga caccaacttc 1140
actgtcacct caaaggctaa tgatgaagaa ggcgactttg ctgagctcta catgttcaag 1200
tggaacgacgc ttcttatccc tccgacgacc attttgatca ttaacatggg cgggtgctgtt 1260
gctgggtacct cctacgccat caacagtggg taccaatcat gggggccgct ctttggggaag 1320
ctcttctttg ccttctgggt gattgttcac ttatacccat tcctcaaggg tcttatgggc 1380
aggcaaaacc gcacaccgac gattgtcatc gtctgggctg tcctcctcgc ttctatcttc 1440
tccttgctgt ggggttcgtg tgatccattc actaccgctc tcgctggccc aaatatccaa 1500
acctgtggca tcaactgcta ggaaagtggg agtttgtaga gacagaaaat ataacagtga 1560
tcgagcgacc acctgtggag ccagagaata tttatgttgg ggttgtgaat tactacgttt 1620
gagaaagttg tcaaaattga gaaaacacat ttgtaaatag atgtaataga ctatctaccg 1680
ttttcatgag gttaagctct tcttttttg aaaaaaaaaa aaaaaaaaaa aaa 1733

```

<210> 20  
 <211> 506  
 <212> PRT  
 <213> *Triticum aestivum*

<220>  
 <221> UNSURE  
 <222> (88)

<400> 20  
 Glu Ala Met Cys Phe Leu Met Asp Pro Asn Leu Gly Pro Gln Val Cys  
 1 5 10 15  
 Tyr Val Gln Phe Pro Gln Arg Phe Asp Gly Ile Asp Arg Asn Asp Arg  
 20 25 30  
 Tyr Ala Asn Arg Asn Thr Val Phe Phe Asp Ile Asn Leu Arg Gly Leu  
 35 40 45  
 Asp Gly Ile Gln Gly Pro Val Tyr Val Gly Thr Gly Cys Val Phe Asn  
 50 55 60  
 Arg Thr Ala Ile Tyr Gly Tyr Glu Pro Pro Ile Lys Ala Lys Lys Pro  
 65 70 75 80  
 Gly Phe Leu Ala Ser Leu Cys Xaa Gly Lys Lys Lys Ala Ser Lys Ser  
 85 90 95  
 Lys Lys Arg Ser Ser Asp Lys Lys Lys Ser Asn Lys His Val Asp Ser  
 100 105 110  
 Ser Val Pro Val Phe Asn Leu Glu Asp Ile Glu Glu Gly Val Glu Gly  
 115 120 125  
 Ala Gly Phe Asp Asp Glu Lys Ser Val Leu Met Ser Gln Met Ser Leu  
 130 135 140  
 Glu Lys Arg Phe Gly Gln Ser Ala Ala Phe Val Ala Ser Thr Leu Met  
 145 150 155 160  
 Glu Tyr Gly Gly Val Pro Gln Ser Ser Thr Pro Glu Ser Leu Leu Lys  
 165 170 175  
 Glu Ala Ile His Val Ile Ser Cys Gly Tyr Glu Asp Lys Ser Glu Trp  
 180 185 190



09000237.070601

Gly	Thr	Glu	Ile	Gly	Trp	Ile	Tyr	Gly	Ser	Val	Thr	Glu	Asp	Ile	Leu	195	200	205
Thr	Gly	Phe	Lys	Met	His	Ala	Arg	Gly	Trp	Arg	Ser	Ile	Tyr	Cys	Met	210	215	220
Pro	Lys	Arg	Pro	Ala	Phe	Lys	Gly	Ser	Ala	Pro	Ile	Asn	Leu	Ser	Asp	225	230	235
Arg	Leu	Asn	Gln	Val	Leu	Arg	Trp	Ala	Leu	Gly	Ser	Val	Glu	Ile	Leu	245	250	255
Phe	Ser	Arg	His	Cys	Pro	Leu	Trp	Tyr	Gly	Tyr	Gly	Gly	Arg	Leu	Lys	260	265	270
Phe	Leu	Glu	Arg	Phe	Ala	Tyr	Ile	Asn	Thr	Thr	Ile	Tyr	Pro	Leu	Thr	275	280	285
Ser	Leu	Pro	Leu	Leu	Val	Tyr	Cys	Ile	Leu	Pro	Ala	Ile	Cys	Leu	Leu	290	295	300
Thr	Gly	Lys	Phe	Ile	Met	Pro	Glu	Ile	Ser	Asn	Leu	Ala	Ser	Ile	Trp	305	310	315
Phe	Ile	Ala	Leu	Phe	Leu	Ser	Ile	Phe	Ala	Thr	Gly	Ile	Leu	Glu	Met	325	330	335
Arg	Trp	Ser	Gly	Val	Gly	Ile	Asp	Glu	Trp	Trp	Arg	Asn	Glu	Gln	Phe	340	345	350
Trp	Val	Ile	Gly	Gly	Ile	Ser	Ala	His	Leu	Phe	Ala	Val	Phe	Gln	Gly	355	360	365
Leu	Leu	Lys	Val	Leu	Ala	Gly	Ile	Asp	Thr	Asn	Phe	Thr	Val	Thr	Ser	370	375	380
Lys	Ala	Asn	Asp	Glu	Glu	Gly	Asp	Phe	Ala	Glu	Leu	Tyr	Met	Phe	Lys	385	390	395
Trp	Thr	Thr	Leu	Leu	Ile	Pro	Pro	Thr	Thr	Ile	Leu	Ile	Ile	Asn	Met	405	410	415
Val	Gly	Val	Val	Ala	Gly	Thr	Ser	Tyr	Ala	Ile	Asn	Ser	Gly	Tyr	Gln	420	425	430
Ser	Trp	Gly	Pro	Leu	Phe	Gly	Lys	Leu	Phe	Phe	Ala	Phe	Trp	Val	Ile	435	440	445
Val	His	Leu	Tyr	Pro	Phe	Leu	Lys	Gly	Leu	Met	Gly	Arg	Gln	Asn	Arg	450	455	460
Thr	Pro	Thr	Ile	Val	Ile	Val	Trp	Ala	Val	Leu	Leu	Ala	Ser	Ile	Phe	465	470	475
Ser	Leu	Leu	Trp	Val	Arg	Val	Asp	Pro	Phe	Thr	Thr	Arg	Leu	Ala	Gly	485	490	495
Pro	Asn	Ile	Gln	Thr	Cys	Gly	Ile	Asn	Cys							500	505	

<210> 21  
 <211> 1029  
 <212> DNA  
 <213> Triticum aestivum

<400> 21  
 gcacgagccg ctcctcacca acggccagat ggttgatgac atccccgccg agcagcacgc 60  
 gctcgtgccg tcctacatga gcggcgggcg cggcgggggc aagaggatcc acccgctccc 120  
 tttcgcagat cccaaccttc cagtgcacc gagatccatg gaccggtcca aggatctggc 180  
 cgacctacgga tatggcagcg tggcctggaa ggagagaatg gagggctgga agcagaagca 240  
 ggagcgccctg cagcatgtca ggagcgaggg tggcggtgat tgggatggcg acgatgcaga 300  
 tctgccacta atggatgaag ctaggcagcc attgtccaga aaagtcccta tatcatcaag 360  
 ccgaattaat ccctacagga tgattatcgt tatccggttg gtggtttttg gtttcttctt 420  
 ccactaccga gtgatgcac cggcgaaaga tgcatttgca ttgtggctca tatctgtaat 480  
 ctgtgaaaatc tggtttgcca tgtcctgtat tcttgatcag ttcccaaagt ggtttccaat 540  
 cgagagagag acttacctgg accgtttgtc actaagggtt gacaaggaag gtcaaccctc 600  
 tcagcttgct ccaatcgact tctttgtcag tacggttgat ccacaaaagg aacctccctt 660  
 ggtcacagcg aacactgtcc ttccatcct tctgtggat tatccggttg agaaggtctc 720  
 ctgctatggt tctgatgatg gtgctgcaat gcttacgttt gaagcattgt ctgaaacatc 780  
 tgaatttgca aagaaatggg ttcctttcag caaaaagttt aatatcgagc ctctgtctcc 840  
 tgagtggtag ttccaacaga agatagacta cctgaaagac aaggttgctg cttcatttgt 900  
 tagggagagg agggcgatga agagagaata cgaggaattc aaggttaagga tcaatgcctt 960  
 ggttgcaaaa gcccaaaagg ttcctgagga aggatggaca atgcaagatg gaagccctg 1020  
 gcctggaaa 1029

<210> 22  
 <211> 340  
 <212> PRT  
 <213> Triticum aestivum

<400> 22  
 Pro Leu Leu Thr Asn Gly Gln Met Val Asp Asp Ile Pro Pro Glu Gln  
 1 5 10 15  
 His Ala Leu Val Pro Ser Tyr Met Ser Gly Gly Gly Gly Gly Lys  
 20 25 30  
 Arg Ile His Pro Leu Pro Phe Ala Asp Pro Asn Leu Pro Val Gln Pro  
 35 40 45  
 Arg Ser Met Asp Pro Ser Lys Asp Leu Ala Ala Tyr Gly Tyr Gly Ser  
 50 55 60  
 Val Ala Trp Lys Glu Arg Met Glu Gly Trp Lys Gln Lys Gln Glu Arg  
 65 70 75 80  
 Leu Gln His Val Arg Ser Glu Gly Gly Gly Asp Trp Asp Gly Asp Asp  
 85 90 95  
 Ala Asp Leu Pro Leu Met Asp Glu Ala Arg Gln Pro Leu Ser Arg Lys  
 100 105 110  
 Val Pro Ile Ser Ser Ser Arg Ile Asn Pro Tyr Arg Met Ile Ile Val  
 115 120 125  
 Ile Arg Leu Val Val Leu Gly Phe Phe Phe His Tyr Arg Val Met His  
 130 135 140  
 Pro Ala Lys Asp Ala Phe Ala Leu Trp Leu Ile Ser Val Ile Cys Glu  
 145 150 155 160

09900237 " 070601

Ile Trp Phe Ala Met Ser Cys Ile Leu Asp Gln Phe Pro Lys Trp Phe  
165 170 175

Pro Ile Glu Arg Glu Thr Tyr Leu Asp Arg Leu Ser Leu Arg Phe Asp  
180 185 190

Lys Glu Gly Gln Pro Ser Gln Leu Ala Pro Ile Asp Phe Phe Val Ser  
195 200 205

Thr Val Asp Pro Thr Lys Glu Pro Pro Leu Val Thr Ala Asn Thr Val  
210 215 220

Leu Ser Ile Leu Ser Val Asp Tyr Pro Val Glu Lys Val Ser Cys Tyr  
225 230 235 240

Val Ser Asp Asp Gly Ala Ala Met Leu Thr Phe Glu Ala Leu Ser Glu  
245 250 255

Thr Ser Glu Phe Ala Lys Lys Trp Val Pro Phe Ser Lys Lys Phe Asn  
260 265 270

Ile Glu Pro Arg Ala Pro Glu Trp Tyr Phe Gln Gln Lys Ile Asp Tyr  
275 280 285

Leu Lys Asp Lys Val Ala Ala Ser Phe Val Arg Glu Arg Arg Ala Met  
290 295 300

Lys Arg Glu Tyr Glu Glu Phe Lys Val Arg Ile Asn Ala Leu Val Ala  
305 310 315 320

Lys Ala Gln Lys Val Pro Glu Glu Gly Trp Thr Met Gln Asp Gly Ser  
325 330 335

Pro Trp Pro Gly  
340

<210> 23  
<211> 2663  
<212> DNA  
<213> Picramnia pentandra

<400> 23

gcacgaggaa	agaggggaag	ccatctgagc	tagctggcct	agacatat	gtcagtacgg	60
tggatcctat	gaaagaacct	ccacttatca	ctgcaaatac	tgtgctatcc	atccttgacg	120
ttgattatcc	agttgataaa	gttacatgct	acgtgtcaga	tgatgggtgct	gccatgctta	180
cttttgaagc	actttctgaa	acatctgaat	ttgcacgaaa	atgggtccct	ttctgtaaga	240
agtttagcat	tgagcctcga	gcaccagaat	ggtatttctc	tcagaagatg	gactatttga	300
agaacaaagt	acacccatca	tttgttaggg	aaagacgtgc	tatgaagaga	gaatatgaag	360
tattcaaagt	tcgataaaat	ggtttggttg	ccatggcaca	aaaggttccc	gaggatgggt	420
ggacgatgca	ggatgggact	ccttggcctg	gaaataatgt	gcgagaccat	cctggcatga	480
ttcaggtttt	ccttggtcac	aatggtgtcc	gtgatgttga	aggaaacgag	ttgcctcgtc	540
tgatatatgt	ttctcgtgag	aagagacctg	gctttgagca	ccataaaaag	gctggtgcaa	600
tgaattcttt	ggtacgggtc	tccgcggtta	tctcaaatgc	accctatata	ctaaacgttg	660
actgtgatca	ttacatcaac	aatagcaaag	cactgagaga	agccatgtgt	ttcatgatgg	720
atccaacatc	ggggaagaaa	ttatgctatg	tgcagtttcc	tcaaagattt	gatggcattg	780
atcgccatga	tcgatattcc	aaccggaatg	ttgtattctt	tgatataaat	atgaaaggat	840
tagatggcat	acaagggcct	atatatgttg	gaacgggatg	tgttttcaga	agagtagcac	900
tttatggcta	tgatgcacca	gtcactaaga	agtcgccggg	aaaagcttgt	aactgttggc	960

```

ctaaatgggtt gtgctgctgt tgtgggtcca gaaagaacaa gaaatcgaaa ccaaagaagg 1020
agaagaagaa gtctaaaaat aggggaagcat caaagcagat acatgctctt gaaaatattg 1080
aagaaggtat gggaggattg aactctgaga aatcatgtga gacaacccca ctgaaattgg 1140
agaagaagtt tggacagtct ccagtgttcg tggcttctac tcttctagaa gatgggtggag 1200
tccctcaaga tgcaactcct gcagcactac tgaaagaagc catacaggtc atcagctgtg 1260
gttatgaaga taaaacagaa tgggggaagg aagttgggtg gatatatggc tctgtaacgg 1320
aggatattct gactggattc aagatgcact gccatggatg gcggtctgtg tactgcatgc 1380
ctgcacgccc cgcatttaag gggtcagctc ccatcaacct ttcagatcgt ctacatcagg 1440
ttcttcggtg ggcccttgga tctgtggaga ttttcttgag cagacattgt ccactctggt 1500
atggctatgg tgggtggatta aaatggttag agcggttttc ctatgtcagt tcggttggtt 1560
atccttggac ctccattcct ttgcttggtt actgcacact gccagccatt tgccttctta 1620
ctgggaaatt cattgttcct gagattagca actatgcaag catcttggtt atgctcctct 1680
tcatatttat tgctgcaacc agcattcttg agatgcaatg ggggtgggtgt ggaatagatg 1740
attggtggag aaatgagcaa ttttgggtca ttggaggtgt ttcacacat ctttttgctc 1800
tcttccaagg tttactgaag gttctggctg gtgtgaacac aaacttctact gttacctcta 1860
aggctgctga tgaaggggat ttctcagagc ttacacctt caagtggaca acctatttaa 1920
ttctccccc aacgttggtg atcataaata ttgttgggtg tgtggttggc gtctccgatg 1980
ccatcaataa tggttatgat tcatggggtc ctttggttgg tcggctatatt ttcgcattct 2040
gggtcattgt ccacctctat cctttcctca agggtttgct tgggaaacaa gatcgcatc 2100
caaccattat tgtggtctgg tctattctgc tggcttcaat tctaaccctt ttgtgggtac 2160
gaataaatcc atttgtgtcg agagatggcc ctgtcttgga agtgtgtggg ttaaattgtg 2220
actaggagac atgaataaaa tggttatgat gttttttttt ggtcaaaatc cctgatgtct 2280
gttgtggagc tatggattat gtctattgat tgcaagtgat gcttgaccg atgcatcact 2340
gggaagatac aattttgtgc aagtttatag gttggtggtg ttagatatt aagatgagga 2400
gggttgacac attgtcattt gttttacaga ttttccatta attcttttat tattttttgt 2460
gggtgtagtt ttttgttgtc ttagcttttt tcttcagatc tctgtatatt ctaagaaata 2520
attgagtcac aatttgtttc attgtcaatg ttttaggaata atttctcatc tgttgtttct 2580
gctgtttcgt cttggaaaca tggacgtgta tgtttctggt atgaagttac tggaatatta 2640
tgggtaaaaa aaaaaaaaaa aaa 2663

```

<210> 24  
 <211> 740  
 <212> PRT  
 <213> *Picramnia pentandra*

<400> 24  
 Thr Arg Lys Glu Gly Lys Pro Ser Glu Leu Ala Gly Leu Asp Ile Phe  
 1 5 10 15  
 Val Ser Thr Val Asp Pro Met Lys Glu Pro Pro Leu Ile Thr Ala Asn  
 20 25 30  
 Thr Val Leu Ser Ile Leu Ala Val Asp Tyr Pro Val Asp Lys Val Thr  
 35 40 45  
 Cys Tyr Val Ser Asp Asp Gly Ala Ala Met Leu Thr Phe Glu Ala Leu  
 50 55 60  
 Ser Glu Thr Ser Glu Phe Ala Arg Lys Trp Val Pro Phe Cys Lys Lys  
 65 70 75 80  
 Phe Ser Ile Glu Pro Arg Ala Pro Glu Trp Tyr Phe Ser Gln Lys Met  
 85 90 95  
 Asp Tyr Leu Lys Asn Lys Val His Pro Ser Phe Val Arg Glu Arg Arg  
 100 105 110  
 Ala Met Lys Arg Glu Tyr Glu Val Phe Lys Val Arg Ile Asn Gly Leu  
 115 120 125

Val	Ala	Met	Ala	Gln	Lys	Val	Pro	Glu	Asp	Gly	Trp	Thr	Met	Gln	Asp
130						135					140				
Gly	Thr	Pro	Trp	Pro	Gly	Asn	Asn	Val	Arg	Asp	His	Pro	Gly	Met	Ile
145					150					155					160
Gln	Val	Phe	Leu	Gly	His	Asn	Gly	Val	Arg	Asp	Val	Glu	Gly	Asn	Glu
				165					170					175	
Leu	Pro	Arg	Leu	Ile	Tyr	Val	Ser	Arg	Glu	Lys	Arg	Pro	Gly	Phe	Glu
			180					185					190		
His	His	Lys	Lys	Ala	Gly	Ala	Met	Asn	Ser	Leu	Val	Arg	Val	Ser	Ala
		195					200					205			
Val	Ile	Ser	Asn	Ala	Pro	Tyr	Ile	Leu	Asn	Val	Asp	Cys	Asp	His	Tyr
	210					215					220				
Ile	Asn	Asn	Ser	Lys	Ala	Leu	Arg	Glu	Ala	Met	Cys	Phe	Met	Met	Asp
225					230					235					240
Pro	Thr	Ser	Gly	Lys	Lys	Leu	Cys	Tyr	Val	Gln	Phe	Pro	Gln	Arg	Phe
				245					250					255	
Asp	Gly	Ile	Asp	Arg	His	Asp	Arg	Tyr	Ser	Asn	Arg	Asn	Val	Val	Phe
			260					265					270		
Phe	Asp	Ile	Asn	Met	Lys	Gly	Leu	Asp	Gly	Ile	Gln	Gly	Pro	Ile	Tyr
		275					280					285			
Val	Gly	Thr	Gly	Cys	Val	Phe	Arg	Arg	Val	Ala	Leu	Tyr	Gly	Tyr	Asp
	290					295					300				
Ala	Pro	Val	Thr	Lys	Lys	Ser	Pro	Gly	Lys	Ala	Cys	Asn	Cys	Trp	Pro
305					310					315					320
Lys	Trp	Leu	Cys	Cys	Cys	Cys	Gly	Ser	Arg	Lys	Asn	Lys	Lys	Ser	Lys
			325						330					335	
Pro	Lys	Lys	Glu	Lys	Lys	Lys	Ser	Lys	Asn	Arg	Glu	Ala	Ser	Lys	Gln
			340					345					350		
Ile	His	Ala	Leu	Glu	Asn	Ile	Glu	Glu	Gly	Met	Gly	Gly	Leu	Asn	Ser
		355					360					365			
Glu	Lys	Ser	Cys	Glu	Thr	Thr	Pro	Leu	Lys	Leu	Glu	Lys	Lys	Phe	Gly
	370					375					380				
Gln	Ser	Pro	Val	Phe	Val	Ala	Ser	Thr	Leu	Leu	Glu	Asp	Gly	Gly	Val
385					390					395					400
Pro	Gln	Asp	Ala	Thr	Pro	Ala	Ala	Leu	Leu	Lys	Glu	Ala	Ile	Gln	Val
				405				410					415		
Ile	Ser	Cys	Gly	Tyr	Glu	Asp	Lys	Thr	Glu	Trp	Gly	Lys	Glu	Val	Gly
			420					425					430		
Trp	Ile	Tyr	Gly	Ser	Val	Thr	Glu	Asp	Ile	Leu	Thr	Gly	Phe	Lys	Met
		435					440					445			

09900237.070601

His	Cys	His	Gly	Trp	Arg	Ser	Val	Tyr	Cys	Met	Pro	Ala	Arg	Pro	Ala	
450						455					460					
Phe	Lys	Gly	Ser	Ala	Pro	Ile	Asn	Leu	Ser	Asp	Arg	Leu	His	Gln	Val	
465					470					475					480	
Leu	Arg	Trp	Ala	Leu	Gly	Ser	Val	Glu	Ile	Phe	Leu	Ser	Arg	His	Cys	
				485					490					495		
Pro	Leu	Trp	Tyr	Gly	Tyr	Gly	Gly	Gly	Leu	Lys	Trp	Leu	Glu	Arg	Phe	
			500					505					510			
Ser	Tyr	Val	Ser	Ser	Val	Val	Tyr	Pro	Trp	Thr	Ser	Ile	Pro	Leu	Leu	
		515					520					525				
Val	Tyr	Cys	Thr	Leu	Pro	Ala	Ile	Cys	Leu	Leu	Thr	Gly	Lys	Phe	Ile	
		530				535					540					
Val	Pro	Glu	Ile	Ser	Asn	Tyr	Ala	Ser	Ile	Leu	Phe	Met	Leu	Leu	Phe	
545					550					555					560	
Ile	Phe	Ile	Ala	Ala	Thr	Ser	Ile	Leu	Glu	Met	Gln	Trp	Gly	Gly	Val	
				565					570					575		
Gly	Ile	Asp	Asp	Trp	Trp	Arg	Asn	Glu	Gln	Phe	Trp	Val	Ile	Gly	Gly	
			580					585					590			
Val	Ser	Ser	His	Leu	Phe	Ala	Leu	Phe	Gln	Gly	Leu	Leu	Lys	Val	Leu	
		595					600					605				
Ala	Gly	Val	Asn	Thr	Asn	Phe	Thr	Val	Thr	Ser	Lys	Ala	Ala	Asp	Glu	
		610				615					620					
Gly	Asp	Phe	Ser	Glu	Leu	Tyr	Leu	Phe	Lys	Trp	Thr	Thr	Leu	Leu	Ile	
625					630				635						640	
Pro	Pro	Thr	Thr	Leu	Leu	Ile	Ile	Asn	Ile	Val	Gly	Val	Val	Val	Gly	
				645				650						655		
Val	Ser	Asp	Ala	Ile	Asn	Asn	Gly	Tyr	Asp	Ser	Trp	Gly	Pro	Leu	Phe	
			660					665					670			
Gly	Arg	Leu	Phe	Phe	Ala	Phe	Trp	Val	Ile	Val	His	Leu	Tyr	Pro	Phe	
		675					680					685				
Leu	Lys	Gly	Leu	Leu	Gly	Lys	Gln	Asp	Arg	Thr	Pro	Thr	Ile	Ile	Val	
		690				695					700					
Val	Trp	Ser	Ile	Leu	Leu	Ala	Ser	Ile	Leu	Thr	Leu	Leu	Trp	Val	Arg	
705					710					715					720	
Ile	Asn	Pro	Phe	Val	Ser	Arg	Asp	Gly	Pro	Val	Leu	Glu	Val	Cys	Gly	
				725					730					735		
Leu	Asn	Cys	Asp													
			740													

<210> 25  
 <211> 3563  
 <212> DNA  
 <213> *Impatiens balsamia*

<400> 25  
 gcacgagagg caaacgccgg actagtgcgc ggatcttaca agcgggaacga gcttgtccga 60  
 attcgccacg attcagatgg cgggcagccg aagcccctaa aagaggctaa cggacagata 120  
 tgtcagatat gcggtgacac agtcggaaaa tcagccaccg gcgacacttt cgttgcctgt 180  
 aatgaatgtg gattccccgt ttgccggcct tgttacgagt acgaaaggaa agatggaaac 240  
 caatgctgcc ctcaagtcaa gaccagatac aaaagacaga aagggaagtcc tagagttgaa 300  
 ggagatgaag aagaggagga tgtggatgat ttggaaaacg agttcaatta ttccggtaaa 360  
 gggagaagacc agaagaaggt aaccacggca aggcggccat ggcagggaga tcagcaggat 420  
 attgagctct ctgtttcatc atctaggcat gatgaatccc aacaacctgt acctcttctc 480  
 actcacgggc actcggtatc gggcgaaatt cccactcccg ataatcattc tataaggact 540  
 acatcaggtc ccataggccc tgtggaaaaa tccattccct atatcgatcc caggcagcca 600  
 gttgctgtga gaataattgt tgacccttcc aaggacttga actcgtagcg gcttggcaat 660  
 gtggattgga aggaaagggt tgaaggttgg aaacttaagc aggagaaaaa tatggtgcaa 720  
 atgaccagta gatatactga agggaaagga gatactgaag gtacgggagc aaatggggag 780  
 gaacttcaaa tggtgcccga cgatatccga caacccatga gccgaatcgt gccatttctg 840  
 tcgacgcacc tcactcccta cagagtgggt atcatacttc gggttaattat cctcggtttc 900  
 ttcttgcaat accgttgtac tcatccagtg aaagatgctt atccattatg gcttacctcg 960  
 gttatttgtg aagtttgggt tgcatgtca tggtgtcttg atcagttccc taaatggctg 1020  
 cctgtgaacc gcgagactta tctcgacaga ctgtccatga gattcgatag ggaaggggag 1080  
 ccttcgcaat tggcgccaat tgacgtattt gttagtaccg tggatccctt gaaagagcca 1140  
 ccaactcgtga cagccaacac ggttttgtct atcctggccg tggattaccc tgttgacaaa 1200  
 gtctcttgct atgtttcggg tgacggttca gcaatgttga ccttcgaagc tctatccgag 1260  
 acagccgagt ttgctaagaa atgggcaccc ttctgtaaga aacatagtat tgaacctcgg 1320  
 gcgcccgaat tttatttcgc tcaaaagatt gattacttga aggataagggt gcagccttct 1380  
 ttcgtgaagg agcggagggc gatgaagagg gaatacgaag aatttaagggt taggattaat 1440  
 gcgcttggtg cgaaagcgca aaaagtgccg gaagaaggat ggacgatgca agatggaact 1500  
 ccatggccgg gaaataactc gagagatcat cctggaatga ttcaggtttt tttaggccat 1560  
 agtggggggt tcgatacggg gggaaatgag ttacctcggc tgggtgtacgt ttctcgtgag 1620  
 aaacgtcctg gatttcagca tcacaagaaa gccggggcaa tgaacgcatt gattcgagta 1680  
 tcggcagtg tgacaaatgg ggcttatctg cttaacgtgg attgtgatca ctacttcaac 1740  
 aacagcaaat gtctaaaaga ggcaatgtgc tttatgatgg atocaaacct tggaaagaaa 1800  
 acatgttacg ttcagttccc tcaacggttt gatgggtatt acttgacga tcgatatgct 1860  
 aaccgtaaca ttgtcttctt cgatatcaac ttgaaagggt tggacggcat tcagggccca 1920  
 gtttatgtgg gtaccggttg ttgtttcaac agacaggcgc tatacgggta tgatccagtc 1980  
 ttaacagagg aggattttgga accgaatatc atcatcaaga gctgttgccg ctcgaggaaa 2040  
 aagggtaaaag gtggcaacaa gaagtacatt gacaaaaaca gagcactaaa gcgaaccgaa 2100  
 tcaaccgcgc ccattttcaa tatggaagat attgaagggt gcattgaagg ttacgatgac 2160  
 gagagatctt ttctcatggc acagagttac gaaaagcggg tcgggtcaatc cctgttctt 2220  
 attgctgcca cgttcatgga acaaggcggc ctctctcctt ccacaaactc tgcaaccctc 2280  
 ttgaaagaag caatccatgt tattagctgt gggtagcagg acaagactga atggggcaaa 2340  
 gagattggat ggatatatgg atctgtaacg gaagatatct tgaccgggtt caagatgcat 2400  
 acgagaggat ggatttcaat ctactgcatg ccgccacgcc ctgccttcaa aggatctgca 2460  
 cccattaatc tttcggatcg tttgaaccag gtcttctgat gggctctcgg atcgattgag 2520  
 attcttttga gtagacattg ccccatttgg tatggctaca gcggtagact caagttcttg 2580  
 gagagattgg cttatatcaa tactattggt tatccactca cctccattcc tttacttgct 2640  
 tattgcaccc ttcctgctat ctgcttactc accggaaagt tcatcgttcc ggagataagc 2700  
 aactacgcga gcatctggtt cattcttctg ttctgtctca ttttctcgac gggataactg 2760  
 gagctaagat ggagcggggt tactctggag gactggtgga gaaacgagca attctgggta 2820  
 atcggtggca cgtcggctca tctctttgcc gtgttccaag gcctgctaaa agtgcttgcg 2880  
 gggatcgaca cgaatttcac cgtcacgtcg aaagcgtcgg acgaggacgg ggaactttgcg 2940  
 gagcttttacg ttttcaagtg gacttccctt ctcatccctc cgaccacat tctggttgtg 3000  
 aacatgggtg ggatagtggc cggcgtctcg ttccgcatca acagtggata ccagtcgtg 3060  
 ggaccgctct tcggaaggtt gttctttgcg atatgggtta ttgtccattt gtaccatttc 3120  
 cttaagggtt tgttgggacg gcagaatcgg acaccacga ttgttattgt ctggtctgta 3180  
 cttttggctt ccataatttc tcttctatgg gtgcgtattg atccgtttac atcggaactcg 3240

```

acaaaggctc gggggcaatg tgggatcgat tgctgagaat tgagattgtc ccgagtctgt 3300
tgttacagta aatagatggg catggccgcc atagagaaga tgaagaaggt aactacttaa 3360
attggcgctc acattttgtt aggcttctgc ccttcacaga caatgagggc caaagtgttt 3420
gatatgtcta ggtattaatg tggtatacca actctaactt aaaacagtgt aatggattcc 3480
agaatgacga atgacttggt cggtttcaat tatttgaatt cctcaaaaac taatatcttt 3540
tccccaaaaa aaaaaaaaaa aaa                                     3563

```

```

<210> 26
<211> 1091
<212> PRT
<213> Impatiens balsamia

```

```

<400> 26
Ala Arg Glu Ala Asn Ala Gly Leu Val Ala Gly Ser Tyr Lys Arg Asn
 1          5          10          15

Glu Leu Val Arg Ile Arg His Asp Ser Asp Gly Gly Gln Pro Lys Pro
          20          25          30

Leu Lys Glu Ala Asn Gly Gln Ile Cys Gln Ile Cys Gly Asp Thr Val
          35          40          45

Gly Lys Ser Ala Thr Gly Asp Thr Phe Val Ala Cys Asn Glu Cys Gly
          50          55          60

Phe Pro Val Cys Arg Pro Cys Tyr Glu Tyr Glu Arg Lys Asp Gly Asn
          65          70          75          80

Gln Cys Cys Pro Gln Cys Lys Thr Arg Tyr Lys Arg Gln Lys Gly Ser
          85          90          95

Pro Arg Val Glu Gly Asp Glu Glu Glu Glu Asp Val Asp Asp Leu Glu
          100          105          110

Asn Glu Phe Asn Tyr Ser Gly Lys Gly Lys Asn Gln Lys Lys Val Thr
          115          120          125

Thr Ala Arg Arg Pro Trp Gln Gly Asp Gln Gln Asp Ile Glu Leu Ser
          130          135          140

Val Ser Ser Ser Arg His Asp Glu Ser Gln Gln Pro Val Pro Leu Leu
          145          150          155          160

Thr His Gly His Ser Val Ser Gly Glu Ile Pro Thr Pro Asp Asn His
          165          170          175

Ser Ile Arg Thr Thr Ser Gly Pro Ile Gly Pro Val Glu Lys Ser Ile
          180          185          190

Pro Tyr Ile Asp Pro Arg Gln Pro Val Ala Val Arg Ile Ile Val Asp
          195          200          205

Pro Ser Lys Asp Leu Asn Ser Tyr Gly Leu Gly Asn Val Asp Trp Lys
          210          215          220

Glu Arg Val Glu Gly Trp Lys Leu Lys Gln Glu Lys Asn Met Val Gln
          225          230          235          240

```



Met	Thr	Ser	Arg	Tyr	Pro	Glu	Gly	Lys	Gly	Asp	Thr	Glu	Gly	Thr	Gly	
				245					250					255		
Ser	Asn	Gly	Glu	Glu	Leu	Gln	Met	Ala	Ala	Asp	Asp	Ile	Arg	Gln	Pro	
			260					265					270			
Met	Ser	Arg	Ile	Val	Pro	Ile	Ser	Ser	Thr	His	Leu	Thr	Pro	Tyr	Arg	
		275					280					285				
Val	Val	Ile	Ile	Leu	Arg	Leu	Ile	Ile	Leu	Gly	Phe	Phe	Leu	Gln	Tyr	
	290					295					300					
Arg	Cys	Thr	His	Pro	Val	Lys	Asp	Ala	Tyr	Pro	Leu	Trp	Leu	Thr	Ser	
305					310					315					320	
Val	Ile	Cys	Glu	Val	Trp	Phe	Ala	Leu	Ser	Trp	Leu	Leu	Asp	Gln	Phe	
				325					330					335		
Pro	Lys	Trp	Ser	Pro	Val	Asn	Arg	Glu	Thr	Tyr	Leu	Asp	Arg	Leu	Ser	
			340					345					350			
Met	Arg	Phe	Asp	Arg	Glu	Gly	Glu	Pro	Ser	Gln	Leu	Ala	Pro	Ile	Asp	
		355					360					365				
Val	Phe	Val	Ser	Thr	Val	Asp	Pro	Leu	Lys	Glu	Pro	Pro	Leu	Val	Thr	
	370					375					380					
Ala	Asn	Thr	Val	Leu	Ser	Ile	Leu	Ala	Val	Asp	Tyr	Pro	Val	Asp	Lys	
385					390					395					400	
Val	Ser	Cys	Tyr	Val	Ser	Asp	Asp	Gly	Ser	Ala	Met	Leu	Thr	Phe	Glu	
				405					410					415		
Ala	Leu	Ser	Glu	Thr	Ala	Glu	Phe	Ala	Lys	Lys	Trp	Ala	Pro	Phe	Cys	
			420					425					430			
Lys	Lys	His	Ser	Ile	Glu	Pro	Arg	Ala	Pro	Glu	Phe	Tyr	Phe	Ala	Gln	
		435					440					445				
Lys	Ile	Asp	Tyr	Leu	Lys	Asp	Lys	Val	Gln	Pro	Ser	Phe	Val	Lys	Glu	
	450					455					460					
Arg	Arg	Ala	Met	Lys	Arg	Glu	Tyr	Glu	Glu	Phe	Lys	Val	Arg	Ile	Asn	
465					470					475					480	
Ala	Leu	Val	Ala	Lys	Ala	Gln	Lys	Val	Pro	Glu	Glu	Gly	Trp	Thr	Met	
				485					490					495		
Gln	Asp	Gly	Thr	Pro	Trp	Pro	Gly	Asn	Asn	Ser	Arg	Asp	His	Pro	Gly	
			500					505					510			
Met	Ile	Gln	Val	Phe	Leu	Gly	His	Ser	Gly	Gly	Phe	Asp	Thr	Glu	Gly	
		515					520					525				
Asn	Glu	Leu	Pro	Arg	Leu	Val	Tyr	Val	Ser	Arg	Glu	Lys	Arg	Pro	Gly	
	530					535					540					
Phe	Gln	His	His	Lys	Lys	Ala	Gly	Ala	Met	Asn	Ala	Leu	Ile	Arg	Val	
545					550					555					560	

09900237 45200660  
T09020

Ser	Ala	Val	Leu	Thr	Asn	Gly	Ala	Tyr	Leu	Leu	Asn	Val	Asp	Cys	Asp	
				565					570					575		
His	Tyr	Phe	Asn	Asn	Ser	Lys	Cys	Leu	Lys	Glu	Ala	Met	Cys	Phe	Met	
			580					585					590			
Met	Asp	Pro	Asn	Leu	Gly	Lys	Lys	Thr	Cys	Tyr	Val	Gln	Phe	Pro	Gln	
		595					600					605				
Arg	Phe	Asp	Gly	Ile	Asp	Leu	His	Asp	Arg	Tyr	Ala	Asn	Arg	Asn	Ile	
	610					615					620					
Val	Phe	Phe	Asp	Ile	Asn	Leu	Lys	Gly	Leu	Asp	Gly	Ile	Gln	Gly	Pro	
625					630					635					640	
Val	Tyr	Val	Gly	Thr	Gly	Cys	Cys	Phe	Asn	Arg	Gln	Ala	Leu	Tyr	Gly	
				645					650					655		
Tyr	Asp	Pro	Val	Leu	Thr	Glu	Glu	Asp	Leu	Glu	Pro	Asn	Ile	Ile	Ile	
			660					665					670			
Lys	Ser	Cys	Cys	Gly	Ser	Arg	Lys	Lys	Gly	Lys	Gly	Gly	Asn	Lys	Lys	
		675					680					685				
Tyr	Ile	Asp	Lys	Asn	Arg	Ala	Leu	Lys	Arg	Thr	Glu	Ser	Thr	Ala	Pro	
	690					695					700					
Ile	Phe	Asn	Met	Glu	Asp	Ile	Glu	Glu	Gly	Ile	Glu	Gly	Tyr	Asp	Asp	
705					710					715					720	
Glu	Arg	Ser	Phe	Leu	Met	Ala	Gln	Ser	Tyr	Glu	Lys	Arg	Phe	Gly	Gln	
				725					730					735		
Ser	Pro	Val	Leu	Ile	Ala	Ala	Thr	Phe	Met	Glu	Gln	Gly	Gly	Leu	Pro	
			740					745					750			
Pro	Ser	Thr	Asn	Ser	Ala	Thr	Leu	Leu	Lys	Glu	Ala	Ile	His	Val	Ile	
		755					760					765				
Ser	Cys	Gly	Tyr	Glu	Asp	Lys	Thr	Glu	Trp	Gly	Lys	Glu	Ile	Gly	Trp	
	770					775					780					
Ile	Tyr	Gly	Ser	Val	Thr	Glu	Asp	Ile	Leu	Thr	Gly	Phe	Lys	Met	His	
785					790					795					800	
Thr	Arg	Gly	Trp	Ile	Ser	Ile	Tyr	Cys	Met	Pro	Pro	Arg	Pro	Ala	Phe	
				805					810					815		
Lys	Gly	Ser	Ala	Pro	Ile	Asn	Leu	Ser	Asp	Arg	Leu	Asn	Gln	Val	Leu	
			820					825					830			
Arg	Trp	Ala	Leu	Gly	Ser	Ile	Glu	Ile	Leu	Leu	Ser	Arg	His	Cys	Pro	
		835					840					845				
Ile	Trp	Tyr	Gly	Tyr	Ser	Gly	Arg	Leu	Lys	Phe	Leu	Glu	Arg	Leu	Ala	
	850					855					860					
Tyr	Ile	Asn	Thr	Ile	Val	Tyr	Pro	Leu	Thr	Ser	Ile	Pro	Leu	Leu	Ala	
865					870					875					880	

Tyr Cys Thr Leu Pro Ala Ile Cys Leu Leu Thr Gly Lys Phe Ile Val  
885 890 895

Pro Glu Ile Ser Asn Tyr Ala Ser Ile Trp Phe Ile Leu Leu Phe Val  
900 905 910

Ser Ile Phe Ser Thr Gly Ile Leu Glu Leu Arg Trp Ser Gly Val Thr  
915 920 925

Leu Glu Asp Trp Trp Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Thr  
930 935 940

Ser Ala His Leu Phe Ala Val Phe Gln Gly Leu Leu Lys Val Leu Ala  
945 950 955 960

Gly Ile Asp Thr Asn Phe Thr Val Thr Ser Lys Ala Ser Asp Glu Asp  
965 970 975

Gly Asp Phe Ala Glu Leu Tyr Val Phe Lys Trp Thr Ser Leu Leu Ile  
980 985 990

Pro Pro Thr Thr Ile Leu Val Val Asn Met Val Gly Ile Val Ala Gly  
995 1000 1005

Val Ser Phe Ala Ile Asn Ser Gly Tyr Gln Ser Trp Gly Pro Leu Phe  
1010 1015 1020

Gly Arg Leu Phe Phe Ala Ile Trp Val Ile Val His Leu Tyr Pro Phe  
1025 1030 1035 1040

Leu Lys Gly Leu Leu Gly Arg Gln Asn Arg Thr Pro Thr Ile Val Ile  
1045 1050 1055

Val Trp Ser Val Leu Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Arg  
1060 1065 1070

Ile Asp Pro Phe Thr Ser Asp Ser Thr Lys Ala Arg Gly Gln Cys Gly  
1075 1080 1085

Ile Asp Cys  
1090

<210> 27  
<211> 1560  
<212> DNA  
<213> Glycine max

<400> 27  
gcacgagggg aaggggaacc atcacagcta gcagctgttg acatttttgt cagtactgtt 60  
gatccattaa aagaaccccc gcttgtgact gctaacactg tcctatctat tctttctgtt 120  
gactaccag tggataaggt ctctgttat gtctctgatg atggtgctgc tatgttgaca 180  
tttgaagctc tggctgagac atcagaattt gctaggaaat gggttccttt cagcaagaaa 240  
tataatatcg aacctcgggc acctgagtgg tattttgcac agaagattga ctacttgaaa 300  
gataaggttc aaccatcatt tgtcaaagat cgtagagcaa tgaagagaga atatgaagaa 360  
tttaaaattc gcatcaatgg acttgttgca aaggcacaaa agattcctga agaaggatgg 420  
gtgatgcaag atggtacgcc atggcctgga aacaacacta gagaccatcc aggaatgatt 480  
caggttttct tgggccaaag tggaggactt gacactgagg gtaatgaact tccacgttta 540  
gtctatgttt ctctgtaaaa gcgtccaggg ttccaacatc acaagaaggc tgggtgcatg 600  
aatgcacttg ttcgagtgtc agcagtcctt actaatggac ctttcttatt gaatcttgat 660

```

tgtgatcact acataaaca cagtaaagcc ttgaggggaag ctatgtgctt tatgatggat 720
cccaaccttg ggaataatgt ttgctatgtc cagtttccac agagggttga tggattgat 780
aggaatgata gatatgcaa tcgcaatact gttttctttg atataaaactt gagagggttg 840
gatggcattc aagggtcctgt ttatgtgggt actggatgtg tctttaatag aacagctttg 900
tatggctacg aacctcctat taaacccaag cataaaaaagc ctgggtttct ttcttcactc 960
tgtgggtgta accgaaagaa gagatcaaaa tctagcaaga aagggtcaga caagaaaaaa 1020
tctagcaaga atgttgaccc aactgtgccc atcttttagtc ttgaggatat agaagagggg 1080
gtggaagggt ctggatttga tgatgagaaa tcaactacta tgtcacaat gagcctcgag 1140
aaaagggttg gtcagtctgc tgtctttgtt gcctctacac tcatggagaa tgggtggcgtt 1200
cctcagtctg caactccaga aactcttctt aaggaagcta ttcattgttat cagttgtggt 1260
tacgaggata aatcagaatg ggggaagtga gtatgagtta ccttatgttt aatgggtctt 1320
tatgtttctt attcccagtc gcattcctgtt atcagattaa tgtagcaga ttagtgtgca 1380
ttcagggacc aaagatccaa tgaattaaac ttaaataatga taaagtatga acagtatagt 1440
actgtctttt ttgagcctaa tatattaccc tctttgtaca gagttaaag gggagcttta 1500
aaatctttcc ttttctaagt aatgtgtgag atttcactag aaaaaaaaaa aaaaaaaaaa 1560

```

<210> 28

<211> 431

<212> PRT

<213> Glycine max

<400> 28

```

Ala Arg Gly Glu Gly Glu Pro Ser Gln Leu Ala Ala Val Asp Ile Phe
  1                      5                      10          15

Val Ser Thr Val Asp Pro Leu Lys Glu Pro Pro Leu Val Thr Ala Asn
          20                      25          30

Thr Val Leu Ser Ile Leu Ser Val Asp Tyr Pro Val Asp Lys Val Ser
          35                      40          45

Cys Tyr Val Ser Asp Asp Gly Ala Ala Met Leu Thr Phe Glu Ala Leu
          50                      55          60

Ala Glu Thr Ser Glu Phe Ala Arg Lys Trp Val Pro Phe Ser Lys Lys
          65                      70          75          80

Tyr Asn Ile Glu Pro Arg Ala Pro Glu Trp Tyr Phe Ala Gln Lys Ile
          85                      90          95

Asp Tyr Leu Lys Asp Lys Val Gln Pro Ser Phe Val Lys Asp Arg Arg
          100                     105          110

Ala Met Lys Arg Glu Tyr Glu Glu Phe Lys Ile Arg Ile Asn Gly Leu
          115                     120          125

Val Ala Lys Ala Gln Lys Ile Pro Glu Glu Gly Trp Val Met Gln Asp
          130                     135          140

Gly Thr Pro Trp Pro Gly Asn Asn Thr Arg Asp His Pro Gly Met Ile
          145                     150          155          160

Gln Val Phe Leu Gly Gln Ser Gly Gly Leu Asp Thr Glu Gly Asn Glu
          165                     170          175

Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Phe Gln
          180                     185          190

```

His His Lys Lys Ala Gly Ala Met Asn Ala Leu Val Arg Val Ser Ala  
195 200 205

Val Leu Thr Asn Gly Pro Phe Leu Leu Asn Leu Asp Cys Asp His Tyr  
210 215 220

Ile Asn Asn Ser Lys Ala Leu Arg Glu Ala Met Cys Phe Met Met Asp  
225 230 235 240

Pro Asn Leu Gly Lys Asn Val Cys Tyr Val Gln Phe Pro Gln Arg Phe  
245 250 255

Asp Gly Ile Asp Arg Asn Asp Arg Tyr Ala Asn Arg Asn Thr Val Phe  
260 265 270

Phe Asp Ile Asn Leu Arg Gly Leu Asp Gly Ile Gln Gly Pro Val Tyr  
275 280 285

Val Gly Thr Gly Cys Val Phe Asn Arg Thr Ala Leu Tyr Gly Tyr Glu  
290 295 300

Pro Pro Ile Lys Pro Lys His Lys Lys Pro Gly Phe Leu Ser Ser Leu  
305 310 315 320

Cys Gly Gly Asn Arg Lys Lys Arg Ser Lys Ser Ser Lys Lys Gly Ser  
325 330 335

Asp Lys Lys Lys Ser Ser Lys Asn Val Asp Pro Thr Val Pro Ile Phe  
340 345 350

Ser Leu Glu Asp Ile Glu Glu Gly Val Glu Gly Ala Gly Phe Asp Asp  
355 360 365

Glu Lys Ser Leu Leu Met Ser Gln Met Ser Leu Glu Lys Arg Phe Gly  
370 375 380

Gln Ser Ala Val Phe Val Ala Ser Thr Leu Met Glu Asn Gly Gly Val  
385 390 395 400

Pro Gln Ser Ala Thr Pro Glu Thr Leu Leu Lys Glu Ala Ile His Val  
405 410 415

Ile Ser Cys Gly Tyr Glu Asp Lys Ser Glu Trp Gly Ser Glu Val  
420 425 430

<210> 29  
<211> 3626  
<212> DNA  
<213> Triticum aestivum

<400> 29  
gcacgaggaa ccccgctcca gctctgtcgt cgggtgcgggt tggatcgctc tgccgcgcca 60  
tggaaggcga cgcggacgcc ctgaagtccg ggaggcacgg ggccggggac gtgtgccaga 120  
tctgcgccga cggcctgggc accacgttgg acggcgacgt cttcaccgcc tgcgacgtct 180  
gccgcttccc ggtctgccgc ccctgctacg agcacgagcg caaggaggggc acccaggcct 240  
gcctccagtg caagaccaag tacaagcgcc acagaggaggg cccagcgatc cgcggggagg 300  
aaggcgacga cactgatgcc gatgatggta gtgacttcaa ctaccctgca tctggcactg 360  
aggaccagaa gcagaagatt gctgacagga tgcgcagctg gcgcatgaac accgggggca 420  
gtggcaatgt tggccacccc aagtatgaca gtggcgagat cggcctctcc aagtatgaca 480

gtggagagat	ccctagggga	tacgtccott	cagtcaccaa	cagccagatg	tcaggagaaa	540
tccctggagc	ttcgccctgat	catcacatga	tgtcccctac	ggggaacatc	agcagacgtg	600
ctccgtttcc	ctatgtgaat	cattcaccaa	atccgtcaag	ggagtctctc	ggcagtattg	660
ggaatggtgc	ctggaaagag	agagttgatg	gctggaaaat	gaagcaggac	aagggtgcga	720
ttcccatgac	taatgggaca	agcattgctc	cctctgaagg	tcgggcagct	actgacatcg	780
atgcatctac	tgaatacaac	atggaagacg	ctttactgaa	tgatgaaact	cgccagcctc	840
tatctagaaa	agtccccatt	gcttccctca	aaataaatcc	ctacagaatg	gtcattgttc	900
tgcggttggt	tgttctaagc	atcttctcgc	actaccgtct	cacaaatcct	gtgcgtaatg	960
cataccacact	gtggctttta	tctgttatat	gtgagatttg	gtttgcttta	tcctggatac	1020
tggatcagtt	cccgaagtgg	tttccaatca	accgggagac	ctaccttgat	agactggctt	1080
taaggtatga	ccgagaaggt	gaaccgtctc	agttggctgc	tggtgacata	tttgtcagta	1140
cagtcgaccc	cttgaaggag	ccacctatcg	tcactgccaa	cactgtgcta	tccattcttg	1200
ctgttgatta	tcccgtggac	aaggctctct	gctatgtatc	tgatgacgga	gcttcaatgc	1260
tgacttttga	cgcattggct	gagacttcag	agtttgctag	gaaatgggta	ccatttgtga	1320
agaagtatga	cattgaaccc	agagctcccc	agttttactt	ttgccagaaa	attgattacc	1380
tgaaagacaa	agtccagcct	tcatttggtta	aagaccgccc	ggccatgaag	agagaatatg	1440
aagaatttaa	aatcaggata	aatgccctag	tttctaaggc	attgaaagtc	cccaggaag	1500
gatggatcat	gcaagatggc	acaccatggc	caggaaacaa	taccagggat	catcctggaa	1560
tgattcaggt	tttccttggt	cacagtgggt	gccttgatac	tgagggtaat	gagctcccc	1620
gtttagttta	tgtgtctcgt	gaaaagcgtc	ctgggttcca	gcaccacaag	aaggctgggtg	1680
ccatgaatgc	ccttgttcgt	gtctcagctg	tccttactaa	tggacaatac	atgttgaatc	1740
ttgatttgta	tcactacatc	aacaacagca	aggctgtccg	agaagctatg	tgcttcctaa	1800
tggatccaaa	cctaggtccg	caagtctggt	atgtgcagtt	cccacaaagg	tttgatggga	1860
ttgataggaa	tgatcgatat	gcaaacagga	acactgtctt	ttttgatatt	aacttgaggg	1920
gccttgacgg	cattcaagga	ccagtttatg	tgggaactgg	ttgtgttttc	aacagaacag	1980
ctatctatgg	ttatgagccc	ccaattaagg	cgaagaagcc	aggtttcttg	gcatcactat	2040
gtgggggcaa	gaagaaggca	agcaagtcaa	agaaaaggag	ctcagataag	aaaaagtcga	2100
acaagcatgt	ggacagttct	gttccagtat	tcaatctcga	agacatagag	gagggtgttg	2160
aagggtgctg	gtttgatgat	gagaaatcag	ttctcatgtc	tcaaatgagc	ttagagaaga	2220
gatttggcca	gtcagcagca	tttgttgcct	ccactctgat	ggaatatggt	ggtgttcctc	2280
agtcctccac	tccagaatct	cttttgaaag	aagctatcca	tgtcataagt	tgtggctatg	2340
aggacaagtc	tgaatgggga	actgagattg	gttggatcta	tgatctgtc	acagaagata	2400
ttcttactgg	attcaagatg	cacgcaagag	gctggcggtc	agtctattgc	atgcccagc	2460
gcccagcttt	caagggatct	gcccccatca	atctttcaga	tcgtctgaac	caagtgtctg	2520
ggtgggctct	cggttctggt	gaaattcttt	tcagccggca	ttgcccttta	tggtatggct	2580
acggagggcg	cctcaagttc	ctggagagat	tcgcttacat	caacaccacc	atttaccac	2640
taacctctct	cccgttctta	gtctattgta	tattgcctgc	tatctgtctg	ctcactggaa	2700
agttcatcat	gccagagatt	agcaacttgg	ccagtatctg	gttcattgctg	ctcttccttt	2760
caattttcgc	cactggtatc	cttgagatga	ggtggagtg	tggtggcatt	gacgagtggt	2820
ggaggaatga	acagttcttg	gtcattggag	gtatctctgc	acatctgttt	gccgtctttc	2880
agggctcttc	gaagggtgct	gccggtatcg	acaccaactt	cactgtcacc	tcaaaggcta	2940
atgacgaaga	aggcgacttt	gctgagctct	acatgttcaa	gtggacgacg	cttctcatcc	3000
ctccgacgac	cattttgatc	attaacatgg	ttggtgtcgt	tgctggcacc	tcctacgcca	3060
tcaacagtgg	ttaccaatca	tgggggcccgc	tctttgggaa	gctcttcttt	gccttctggg	3120
tgattgttca	cttataccca	ttcctcaagg	gtcttatggg	caggcaaaac	cgcacaccga	3180
cgattgtcat	cgtctgggct	gtcctcctcg	cttctatctt	ctccttgctg	tgggttcgtg	3240
ttgatccatt	cactaccgct	ctcgtctggc	caaatatcca	aacctgtggc	atcaactgct	3300
aggaaaagtgg	gagttttag	agacagaaaa	tataacagtg	atcgagcaac	aaccgcgga	3360
gccagagaat	atttatgttg	gggttgtgaa	ttactacgtt	tgagaaaagt	gtcaaaattg	3420
agaaaacaca	tttgtaaata	gatgtaatat	accactaccc	gttttcatga	ggttaagctc	3480
ttcttttttt	ggaacaaaag	aatctcattg	gtaaacctat	aggaattttc	ctatgaggca	3540
cttttgattg	taggaatgga	cctatgaaat	gttgtattta	ttatttatat	aaattattcc	3600
tgtccttcac	attttgagg	agtttt				3626

<210> 30  
 <211> 1080  
 <212> PRT  
 <213> Triticum aestivum

<400> 30

Met	Asp	Gly	Asp	Ala	Asp	Ala	Leu	Lys	Ser	Gly	Arg	His	Gly	Ala	Gly	
1				5					10					15		
Asp	Val	Cys	Gln	Ile	Cys	Ala	Asp	Gly	Leu	Gly	Thr	Thr	Leu	Asp	Gly	
			20					25					30			
Asp	Val	Phe	Thr	Ala	Cys	Asp	Val	Cys	Arg	Phe	Pro	Val	Cys	Arg	Pro	
		35					40					45				
Cys	Tyr	Glu	His	Glu	Arg	Lys	Glu	Gly	Thr	Gln	Ala	Cys	Leu	Gln	Cys	
	50					55					60					
Lys	Thr	Lys	Tyr	Lys	Arg	His	Arg	Gly	Ser	Pro	Ala	Ile	Arg	Gly	Glu	
65					70					75					80	
Glu	Gly	Asp	Asp	Thr	Asp	Ala	Asp	Asp	Gly	Ser	Asp	Phe	Asn	Tyr	Pro	
				85					90					95		
Ala	Ser	Gly	Thr	Glu	Asp	Gln	Lys	Gln	Lys	Ile	Ala	Asp	Arg	Met	Arg	
			100					105					110			
Ser	Trp	Arg	Met	Asn	Thr	Gly	Gly	Ser	Gly	Asn	Val	Gly	His	Pro	Lys	
		115					120					125				
Tyr	Asp	Ser	Gly	Glu	Ile	Gly	Leu	Ser	Lys	Tyr	Asp	Ser	Gly	Glu	Ile	
	130					135					140					
Pro	Arg	Gly	Tyr	Val	Pro	Ser	Val	Thr	Asn	Ser	Gln	Met	Ser	Gly	Glu	
145					150					155					160	
Ile	Pro	Gly	Ala	Ser	Pro	Asp	His	His	Met	Met	Ser	Pro	Thr	Gly	Asn	
				165					170					175		
Ile	Ser	Arg	Arg	Ala	Pro	Phe	Pro	Tyr	Val	Asn	His	Ser	Pro	Asn	Pro	
			180					185					190			
Ser	Arg	Glu	Phe	Ser	Gly	Ser	Ile	Gly	Asn	Val	Ala	Trp	Lys	Glu	Arg	
		195					200				205					
Val	Asp	Gly	Trp	Lys	Met	Lys	Gln	Asp	Lys	Gly	Ala	Ile	Pro	Met	Thr	
	210					215					220					
Asn	Gly	Thr	Ser	Ile	Ala	Pro	Ser	Glu	Gly	Arg	Ala	Ala	Thr	Asp	Ile	
225					230					235					240	
Asp	Ala	Ser	Thr	Glu	Tyr	Asn	Met	Glu	Asp	Ala	Leu	Leu	Asn	Asp	Glu	
				245					250					255		
Thr	Arg	Gln	Pro	Leu	Ser	Arg	Lys	Val	Pro	Ile	Ala	Ser	Ser	Lys	Ile	
			260					265					270			
Asn	Pro	Tyr	Arg	Met	Val	Ile	Val	Leu	Arg	Leu	Val	Val	Leu	Ser	Ile	
		275					280					285				
Phe	Leu	His	Tyr	Arg	Leu	Thr	Asn	Pro	Val	Arg	Asn	Ala	Tyr	Pro	Leu	
	290					295					300					
Trp	Leu	Leu	Ser	Val	Ile	Cys	Glu	Ile	Trp	Phe	Ala	Leu	Ser	Trp	Ile	
305					310					315					320	

Leu Asp Gln Phe Pro Lys Trp Phe Pro Ile Asn Arg Glu Thr Tyr Leu  
 325 330 335  
 Asp Arg Leu Ala Leu Arg Tyr Asp Arg Glu Gly Glu Pro Ser Gln Leu  
 340 345 350  
 Ala Ala Val Asp Ile Phe Val Ser Thr Val Asp Pro Leu Lys Glu Pro  
 355 360 365  
 Pro Ile Val Thr Ala Asn Thr Val Leu Ser Ile Leu Ala Val Asp Tyr  
 370 375 380  
 Pro Val Asp Lys Val Ser Cys Tyr Val Ser Asp Asp Gly Ala Ser Met  
 385 390 395 400  
 Leu Thr Phe Asp Ala Leu Ala Glu Thr Ser Glu Phe Ala Arg Lys Trp  
 405 410 415  
 Val Pro Phe Val Lys Lys Tyr Asp Ile Glu Pro Arg Ala Pro Glu Phe  
 420 425 430  
 Tyr Phe Cys Gln Lys Ile Asp Tyr Leu Lys Asp Lys Val Gln Pro Ser  
 435 440 445  
 Phe Val Lys Asp Arg Arg Ala Met Lys Arg Glu Tyr Glu Glu Phe Lys  
 450 455 460  
 Ile Arg Ile Asn Ala Leu Val Ser Lys Ala Leu Lys Val Pro Glu Glu  
 465 470 475 480  
 Gly Trp Ile Met Gln Asp Gly Thr Pro Trp Pro Gly Asn Asn Thr Arg  
 485 490 495  
 Asp His Pro Gly Met Ile Gln Val Phe Leu Gly His Ser Gly Gly Leu  
 500 505 510  
 Asp Thr Glu Gly Asn Glu Leu Pro Arg Leu Val Tyr Val Ser Arg Glu  
 515 520 525  
 Lys Arg Pro Gly Phe Gln His His Lys Lys Ala Gly Ala Met Asn Ala  
 530 535 540  
 Leu Val Arg Val Ser Ala Val Leu Thr Asn Gly Gln Tyr Met Leu Asn  
 545 550 555 560  
 Leu Asp Cys Asp His Tyr Ile Asn Asn Ser Lys Ala Val Arg Glu Ala  
 565 570 575  
 Met Cys Phe Leu Met Asp Pro Asn Leu Gly Pro Gln Val Cys Tyr Val  
 580 585 590  
 Gln Phe Pro Gln Arg Phe Asp Gly Ile Asp Arg Asn Asp Arg Tyr Ala  
 595 600 605  
 Asn Arg Asn Thr Val Phe Phe Asp Ile Asn Leu Arg Gly Leu Asp Gly  
 610 615 620  
 Ile Gln Gly Pro Val Tyr Val Gly Thr Gly Cys Val Phe Asn Arg Thr  
 625 630 635 640



Ala	Ile	Tyr	Gly	Tyr	Glu	Pro	Pro	Ile	Lys	Ala	Lys	Lys	Pro	Gly	Phe	
				645					650					655		
Leu	Ala	Ser	Leu	Cys	Gly	Gly	Lys	Lys	Lys	Ala	Ser	Lys	Ser	Lys	Lys	
			660					665					670			
Arg	Ser	Ser	Asp	Lys	Lys	Lys	Ser	Asn	Lys	His	Val	Asp	Ser	Ser	Val	
		675					680					685				
Pro	Val	Phe	Asn	Leu	Glu	Asp	Ile	Glu	Glu	Gly	Val	Glu	Gly	Ala	Gly	
	690					695					700					
Phe	Asp	Asp	Glu	Lys	Ser	Val	Leu	Met	Ser	Gln	Met	Ser	Leu	Glu	Lys	
705					710					715					720	
Arg	Phe	Gly	Gln	Ser	Ala	Ala	Phe	Val	Ala	Ser	Thr	Leu	Met	Glu	Tyr	
				725					730					735		
Gly	Gly	Val	Pro	Gln	Ser	Ser	Thr	Pro	Glu	Ser	Leu	Leu	Lys	Glu	Ala	
			740					745					750			
Ile	His	Val	Ile	Ser	Cys	Gly	Tyr	Glu	Asp	Lys	Ser	Glu	Trp	Gly	Thr	
		755					760					765				
Glu	Ile	Gly	Trp	Ile	Tyr	Gly	Ser	Val	Thr	Glu	Asp	Ile	Leu	Thr	Gly	
	770					775					780					
Phe	Lys	Met	His	Ala	Arg	Gly	Trp	Arg	Ser	Val	Tyr	Cys	Met	Pro	Lys	
785					790					795					800	
Arg	Pro	Ala	Phe	Lys	Gly	Ser	Ala	Pro	Ile	Asn	Leu	Ser	Asp	Arg	Leu	
				805					810					815		
Asn	Gln	Val	Leu	Arg	Trp	Ala	Leu	Gly	Ser	Val	Glu	Ile	Leu	Phe	Ser	
			820					825					830			
Arg	His	Cys	Pro	Leu	Trp	Tyr	Gly	Tyr	Gly	Gly	Arg	Leu	Lys	Phe	Leu	
		835					840					845				
Glu	Arg	Phe	Ala	Tyr	Ile	Asn	Thr	Thr	Ile	Tyr	Pro	Leu	Thr	Ser	Leu	
	850					855					860					
Pro	Leu	Leu	Val	Tyr	Cys	Ile	Leu	Pro	Ala	Ile	Cys	Leu	Leu	Thr	Gly	
865					870					875					880	
Lys	Phe	Ile	Met	Pro	Glu	Ile	Ser	Asn	Leu	Ala	Ser	Ile	Trp	Phe	Ile	
				885					890					895		
Ala	Leu	Phe	Leu	Ser	Ile	Phe	Ala	Thr	Gly	Ile	Leu	Glu	Met	Arg	Trp	
			900					905					910			
Ser	Gly	Val	Gly	Ile	Asp	Glu	Trp	Trp	Arg	Asn	Glu	Gln	Phe	Trp	Val	
		915					920					925				
Ile	Gly	Gly	Ile	Ser	Ala	His	Leu	Phe	Ala	Val	Phe	Gln	Gly	Leu	Leu	
	930					935					940					
Lys	Val	Leu	Ala	Gly	Ile	Asp	Thr	Asn	Phe	Thr	Val	Thr	Ser	Lys	Ala	
945					950					955					960	

Asn Asp Glu Glu Gly Asp Phe Ala Glu Leu Tyr Met Phe Lys Trp Thr  
 965 970 975  
 Thr Leu Leu Ile Pro Pro Thr Thr Ile Leu Ile Ile Asn Met Val Gly  
 980 985 990  
 Val Val Ala Gly Thr Ser Tyr Ala Ile Asn Ser Gly Tyr Gln Ser Trp  
 995 1000 1005  
 Gly Pro Leu Phe Gly Lys Leu Phe Phe Ala Phe Trp Val Ile Val His  
 1010 1015 1020  
 Leu Tyr Pro Phe Leu Lys Gly Leu Met Gly Arg Gln Asn Arg Thr Pro  
 1025 1030 1035 1040  
 Thr Ile Val Ile Val Trp Ala Val Leu Leu Ala Ser Ile Phe Ser Leu  
 1045 1050 1055  
 Leu Trp Val Arg Val Asp Pro Phe Thr Thr Arg Leu Ala Gly Pro Asn  
 1060 1065 1070  
 Ile Gln Thr Cys Gly Ile Asn Cys  
 1075 1080  
 <210> 31  
 <211> 685  
 <212> PRT  
 <213> Gossypium hirsutum  
 <400> 31  
 Arg Arg Trp Val Pro Phe Cys Lys Lys His Asn Val Glu Pro Arg Ala  
 1 5 10 15  
 Pro Glu Phe Tyr Phe Asn Glu Lys Ile Asp Tyr Leu Lys Asp Lys Val  
 20 25 30  
 His Pro Ser Phe Val Lys Glu Arg Arg Ala Met Lys Arg Glu Tyr Glu  
 35 40 45  
 Glu Phe Lys Val Arg Ile Asn Ala Leu Val Ala Lys Ala Gln Lys Lys  
 50 55 60  
 Pro Glu Glu Gly Trp Val Met Gln Asp Gly Thr Pro Trp Pro Gly Asn  
 65 70 75 80  
 Asn Thr Arg Asp His Pro Gly Met Ile Gln Val Tyr Leu Gly Ser Ala  
 85 90 95  
 Gly Ala Leu Asp Val Asp Gly Lys Glu Leu Pro Arg Leu Val Tyr Val  
 100 105 110  
 Ser Arg Glu Lys Arg Pro Gly Tyr Gln His His Lys Lys Ala Gly Ala  
 115 120 125  
 Glu Asn Ala Leu Val Arg Val Ser Ala Val Leu Thr Asn Ala Pro Phe  
 130 135 140

09900237.070501

Ile	Leu	Asn	Leu	Asp	Cys	Asp	His	Tyr	Ile	Asn	Asn	Ser	Lys	Ala	Met	
145					150					155					160	
Arg	Glu	Ala	Met	Cys	Phe	Leu	Met	Asp	Pro	Gln	Phe	Gly	Lys	Lys	Leu	
				165					170					175		
Cys	Tyr	Val	Gln	Phe	Pro	Gln	Arg	Phe	Asp	Gly	Ile	Asp	Arg	His	Asp	
			180					185					190			
Arg	Tyr	Ala	Asn	Arg	Asn	Val	Val	Phe	Phe	Asp	Ile	Asn	Met	Leu	Gly	
		195					200					205				
Leu	Asp	Gly	Leu	Gln	Gly	Pro	Val	Tyr	Val	Gly	Thr	Gly	Cys	Val	Phe	
	210					215					220					
Asn	Arg	Gln	Ala	Leu	Tyr	Gly	Tyr	Asp	Pro	Pro	Val	Ser	Glu	Lys	Arg	
225					230					235					240	
Pro	Lys	Met	Thr	Cys	Asp	Cys	Trp	Pro	Ser	Trp	Cys	Cys	Cys	Cys	Cys	
				245					250					255		
Gly	Gly	Ser	Arg	Lys	Lys	Ser	Lys	Lys	Lys	Gly	Glu	Lys	Lys	Gly	Leu	
			260					265					270			
Leu	Gly	Gly	Leu	Leu	Tyr	Gly	Lys	Lys	Lys	Lys	Met	Met	Gly	Lys	Asn	
		275					280					285				
Tyr	Val	Lys	Lys	Gly	Ser	Ala	Pro	Val	Phe	Asp	Leu	Glu	Glu	Ile	Glu	
	290					295					300					
Glu	Gly	Leu	Glu	Gly	Tyr	Glu	Glu	Leu	Glu	Lys	Ser	Thr	Leu	Met	Ser	
305					310					315					320	
Gln	Lys	Asn	Phe	Glu	Lys	Arg	Phe	Gly	Gln	Ser	Pro	Val	Phe	Ile	Ala	
				325					330					335		
Ser	Thr	Leu	Met	Glu	Asn	Gly	Gly	Leu	Pro	Glu	Gly	Thr	Asn	Ser	Thr	
			340					345					350			
Ser	Leu	Ile	Lys	Glu	Ala	Ile	His	Val	Ile	Ser	Cys	Gly	Tyr	Glu	Glu	
		355					360					365				
Lys	Thr	Glu	Trp	Gly	Lys	Glu	Ile	Gly	Trp	Ile	Tyr	Gly	Ser	Val	Thr	
	370					375					380					
Glu	Asp	Ile	Leu	Thr	Gly	Phe	Lys	Met	His	Cys	Arg	Gly	Trp	Lys	Ser	
385					390					395					400	
Val	Tyr	Cys	Val	Pro	Lys	Arg	Pro	Ala	Phe	Lys	Gly	Ser	Ala	Pro	Ile	
				405					410					415		
Asn	Leu	Ser	Asp	Arg	Leu	His	Gln	Val	Leu	Arg	Trp	Ala	Leu	Gly	Ser	
			420					425					430			
Val	Glu	Ile	Phe	Leu	Ser	Arg	His	Cys	Pro	Leu	Trp	Tyr	Gly	Tyr	Gly	
		435					440					445				
Gly	Lys	Leu	Lys	Trp	Leu	Glu	Arg	Leu	Ala	Tyr	Ile	Asn	Thr	Ile	Val	
	450					455					460					

09900237 " 070601

Tyr Pro Phe Thr Ser Ile Pro Leu Leu Ala Tyr Cys Thr Ile Pro Ala  
465 470 475 480

Val Cys Leu Leu Thr Gly Lys Phe Ile Ile Pro Thr Leu Ser Asn Leu  
485 490 495

Thr Ser Val Trp Phe Leu Ala Leu Phe Leu Ser Ile Ile Ala Thr Gly  
500 505 510

Val Leu Glu Leu Arg Trp Ser Gly Val Ser Ile Gln Asp Trp Trp Arg  
515 520 525

Asn Glu Gln Phe Trp Val Ile Gly Gly Val Ser Ala His Leu Phe Ala  
530 535 540

Val Phe Gln Gly Leu Leu Lys Val Leu Ala Gly Val Asp Thr Asn Phe  
545 550 555 560

Thr Val Thr Ala Lys Ala Ala Asp Asp Thr Glu Phe Gly Glu Leu Tyr  
565 570 575

Leu Phe Lys Trp Thr Thr Leu Leu Ile Pro Pro Thr Thr Leu Ile Ile  
580 585 590

Leu Asn Met Val Gly Val Val Ala Gly Val Ser Asp Ala Ile Asn Asn  
595 600 605

Gly Tyr Gly Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe Ala Phe  
610 615 620

Trp Val Ile Leu His Leu Tyr Pro Phe Leu Lys Gly Leu Met Gly Arg  
625 630 635 640

Gln Asn Arg Thr Pro Thr Ile Val Val Leu Trp Ser Ile Leu Leu Ala  
645 650 655

Ser Ile Phe Ser Leu Val Trp Val Arg Ile Asp Pro Phe Leu Pro Lys  
660 665 670

Gln Thr Gly Pro Val Leu Lys Gln Cys Gly Val Glu Cys  
675 680 685

<210> 32  
<211> 701  
<212> PRT  
<213> Gossypium hirsutum

<400> 32  
Asp Tyr Pro Val Glu Lys Val Ser Cys Tyr Val Ser Asp Asp Gly Ala  
1 5 10 15

Ala Met Leu Thr Phe Glu Ala Leu Ser Glu Thr Ser Glu Phe Ala Arg  
20 25 30

Lys Trp Val Pro Phe Cys Lys Lys Tyr Asn Ile Glu Pro Arg Ala Pro  
35 40 45

Glu Trp Tyr Phe Ala Gln Lys Ile Asp Tyr Leu Lys Asp Lys Val Gln  
50 55 60

Thr	Ser	Phe	Val	Lys	Glu	Arg	Arg	Ala	Met	Lys	Arg	Glu	Tyr	Glu	Glu	65	70	75	80
Phe	Lys	Val	Arg	Val	Asn	Gly	Leu	Val	Ala	Lys	Ala	Gln	Lys	Val	Pro	85	90	95	
Glu	Glu	Gly	Trp	Ile	Met	Gln	Asp	Gly	Thr	Pro	Trp	Pro	Gly	Asn	Asn	100	105	110	
Thr	Arg	Asp	His	Pro	Gly	Met	Ile	Gln	Val	Phe	Leu	Gly	Gln	Ser	Gly	115	120	125	
Gly	Leu	Asp	Ala	Glu	Gly	Asn	Glu	Leu	Pro	Arg	Leu	Val	Tyr	Val	Ser	130	135	140	
Arg	Glu	Lys	Arg	Pro	Gly	Phe	Gln	His	His	Lys	Lys	Ala	Gly	Ala	Met	145	150	155	160
Asn	Ala	Leu	Val	Arg	Val	Ser	Ala	Val	Leu	Thr	Asn	Gly	Ala	Phe	Leu	165	170	175	
Leu	Asn	Leu	Asp	Cys	Asp	His	Tyr	Ile	Asn	Asn	Ser	Lys	Ala	Leu	Arg	180	185	190	
Glu	Ala	Met	Cys	Phe	Leu	Met	Asp	Pro	Asn	Leu	Gly	Lys	Gln	Val	Cys	195	200	205	
Tyr	Val	Gln	Phe	Pro	Gln	Arg	Phe	Asp	Gly	Ile	Asp	Arg	Asn	Asp	Arg	210	215	220	
Tyr	Ala	Asn	Arg	Asn	Thr	Val	Phe	Phe	Asp	Ile	Asn	Leu	Arg	Gly	Leu	225	230	235	240
Asp	Gly	Ile	Gln	Gly	Pro	Val	Tyr	Val	Gly	Thr	Gly	Cys	Val	Phe	Asn	245	250	255	
Arg	Thr	Ala	Leu	Tyr	Gly	Tyr	Glu	Pro	Pro	Leu	Lys	Pro	Lys	His	Arg	260	265	270	
Lys	Thr	Gly	Ile	Leu	Ser	Ser	Leu	Cys	Gly	Gly	Ser	Arg	Lys	Lys	Ser	275	280	285	
Ser	Lys	Ser	Ser	Lys	Lys	Gly	Ser	Asp	Lys	Lys	Lys	Ser	Gly	Lys	His	290	295	300	
Val	Asp	Ser	Thr	Val	Pro	Val	Phe	Asn	Leu	Glu	Asp	Ile	Glu	Glu	Gly	305	310	315	320
Val	Glu	Gly	Ala	Gly	Phe	Asp	Asp	Glu	Lys	Ser	Leu	Leu	Met	Ser	Gln	325	330	335	
Met	Ser	Leu	Glu	Lys	Arg	Phe	Gly	Gln	Ser	Ala	Val	Phe	Val	Ala	Ser	340	345	350	
Thr	Leu	Met	Glu	Asn	Gly	Gly	Val	Pro	Gln	Ser	Ala	Thr	Pro	Glu	Thr	355	360	365	
Leu	Leu	Lys	Glu	Ala	Ile	His	Val	Ile	Ser	Cys	Gly	Tyr	Glu	Asp	Lys	370	375	380	

Thr	Asp	Trp	Gly	Ser	Glu	Ile	Gly	Trp	Ile	Tyr	Gly	Ser	Val	Thr	Glu	385	390	395	400
Asp	Ile	Leu	Thr	Gly	Phe	Lys	Met	His	Ala	Arg	Gly	Trp	Arg	Ser	Ile	405	410	415	
Tyr	Cys	Met	Pro	Lys	Arg	Pro	Ala	Phe	Lys	Gly	Ser	Ala	Pro	Ile	Asn	420	425	430	
Leu	Ser	Asp	Arg	Leu	Asn	Gln	Val	Leu	Arg	Trp	Ala	Leu	Gly	Ser	Val	435	440	445	
Glu	Ile	Leu	Phe	Ser	Arg	His	Cys	Pro	Ile	Trp	Tyr	Gly	Tyr	Ser	Gly	450	455	460	
Arg	Leu	Lys	Trp	Leu	Glu	Arg	Phe	Ala	Tyr	Val	Asn	Thr	Thr	Ile	Tyr	465	470	475	480
Pro	Val	Thr	Ala	Ile	Pro	Leu	Leu	Met	Tyr	Cys	Thr	Leu	Pro	Ala	Val	485	490	495	
Cys	Leu	Leu	Thr	Asn	Lys	Phe	Ile	Ile	Pro	Gln	Ile	Ser	Asn	Leu	Ala	500	505	510	
Ser	Ile	Trp	Phe	Ile	Ser	Leu	Phe	Leu	Ser	Ile	Phe	Ala	Thr	Gly	Ile	515	520	525	
Leu	Lys	Met	Lys	Trp	Asn	Gly	Val	Gly	Ile	Asp	Gln	Trp	Trp	Arg	Asn	530	535	540	
Glu	Gln	Phe	Trp	Val	Ile	Gly	Gly	Val	Ser	Ala	His	Leu	Phe	Ala	Val	545	550	555	560
Phe	Gln	Gly	Leu	Leu	Lys	Val	Leu	Ala	Gly	Ile	Asp	Thr	Asn	Phe	Thr	565	570	575	
Val	Thr	Ser	Lys	Ala	Ser	Asp	Glu	Asp	Gly	Asp	Phe	Ala	Glu	Leu	Tyr	580	585	590	
Met	Phe	Lys	Trp	Thr	Thr	Leu	Leu	Ile	Pro	Pro	Thr	Thr	Leu	Leu	Ile	595	600	605	
Ile	Asn	Leu	Val	Gly	Val	Val	Ala	Gly	Ile	Ser	Tyr	Val	Ile	Asn	Ser	610	615	620	
Gly	Tyr	Gln	Ser	Trp	Gly	Pro	Leu	Phe	Gly	Lys	Leu	Phe	Phe	Ala	Phe	625	630	635	640
Trp	Val	Ile	Ile	His	Leu	Tyr	Pro	Phe	Leu	Lys	Gly	Leu	Met	Gly	Arg	645	650	655	
Gln	Asn	Arg	Thr	Pro	Thr	Ile	Val	Val	Val	Trp	Ser	Ile	Leu	Leu	Ala	660	665	670	
Ser	Ile	Phe	Ser	Leu	Leu	Trp	Val	Arg	Ile	Asp	Pro	Phe	Thr	Thr	Arg	675	680	685	
Val	Thr	Gly	Pro	Asp	Val	Glu	Gln	Cys	Gly	Ile	Asn	Cys				690	695	700	

<210> 33  
 <211> 1065  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 33  
 Met Glu Ser Glu Gly Glu Thr Ala Gly Lys Pro Met Lys Asn Ile Val  
   1                  5                  10                  15  
 Pro Gln Thr Cys Gln Ile Cys Ser Asp Asn Val Gly Lys Thr Val Asp  
                   20                  25                  30  
 Gly Asp Arg Phe Val Ala Cys Asp Ile Cys Ser Phe Pro Val Cys Arg  
                   35                  40                  45  
 Pro Cys Tyr Glu Tyr Glu Arg Lys Asp Gly Asn Gln Ser Cys Pro Gln  
           50                  55                  60  
 Cys Lys Thr Arg Tyr Lys Arg Leu Lys Gly Ser Pro Ala Ile Pro Gly  
   65                  70                  75                  80  
 Asp Lys Asp Glu Asp Gly Leu Ala Asp Glu Gly Thr Val Glu Phe Asn  
                   85                  90                  95  
 Tyr Pro Gln Lys Glu Lys Ile Ser Glu Arg Met Leu Gly Trp His Leu  
                   100                  105                  110  
 Thr Arg Gly Lys Gly Glu Glu Met Gly Glu Pro Gln Tyr Asp Lys Glu  
           115                  120                  125  
 Val Ser His Asn His Leu Pro Arg Leu Thr Ser Arg Gln Asp Thr Ser  
   130                  135                  140  
 Gly Glu Phe Ser Ala Ala Ser Pro Glu Arg Leu Ser Val Ser Ser Thr  
  145                  150                  155                  160  
 Ile Ala Gly Gly Lys Arg Leu Pro Tyr Ser Ser Asp Val Asn Gln Ser  
                   165                  170                  175  
 Pro Asn Arg Arg Ile Val Asp Pro Val Gly Leu Gly Asn Val Ala Trp  
                   180                  185                  190  
 Lys Glu Arg Val Asp Gly Trp Lys Met Lys Gln Glu Lys Asn Thr Gly  
           195                  200                  205  
 Pro Val Ser Thr Gln Ala Ala Ser Glu Arg Gly Gly Val Asp Ile Asp  
   210                  215                  220  
 Ala Ser Thr Asp Ile Leu Ala Asp Glu Ala Leu Leu Asn Asp Glu Ala  
  225                  230                  235                  240  
 Arg Gln Pro Leu Ser Arg Lys Val Ser Ile Pro Ser Ser Arg Ile Asn  
                   245                  250                  255  
 Pro Tyr Arg Met Val Ile Met Leu Arg Leu Val Ile Leu Cys Leu Phe  
           260                  265                  270

0900237.070601

Leu	His	Tyr	Arg	Ile	Thr	Asn	Pro	Val	Pro	Asn	Ala	Phe	Ala	Leu	Trp	275	280	285
Leu	Val	Ser	Val	Ile	Cys	Glu	Ile	Trp	Phe	Ala	Leu	Ser	Trp	Ile	Leu	290	295	300
Asp	Gln	Phe	Pro	Lys	Trp	Phe	Pro	Val	Asn	Arg	Glu	Thr	Tyr	Leu	Asp	305	310	315
Arg	Leu	Ala	Leu	Arg	Tyr	Asp	Arg	Glu	Gly	Glu	Pro	Ser	Gln	Leu	Ala	325	330	335
Ala	Val	Asp	Ile	Phe	Val	Ser	Thr	Val	Asp	Pro	Leu	Lys	Glu	Pro	Pro	340	345	350
Leu	Val	Thr	Ala	Asn	Thr	Val	Leu	Ser	Ile	Leu	Ala	Val	Asp	Tyr	Pro	355	360	365
Val	Asp	Lys	Val	Ser	Cys	Tyr	Val	Phe	Asp	Asp	Gly	Ala	Ala	Met	Leu	370	375	380
Ser	Phe	Glu	Ser	Leu	Ala	Glu	Thr	Ser	Glu	Phe	Ala	Arg	Lys	Trp	Val	385	390	395
Pro	Phe	Cys	Lys	Lys	Tyr	Ser	Ile	Glu	Pro	Arg	Ala	Pro	Glu	Trp	Tyr	405	410	415
Phe	Ala	Ala	Lys	Ile	Asp	Tyr	Leu	Lys	Asp	Lys	Val	Gln	Thr	Ser	Phe	420	425	430
Val	Lys	Asp	Arg	Arg	Ala	Met	Lys	Arg	Glu	Tyr	Glu	Glu	Phe	Lys	Ile	435	440	445
Arg	Ile	Asn	Ala	Leu	Val	Ser	Lys	Ala	Leu	Lys	Cys	Pro	Glu	Glu	Gly	450	455	460
Trp	Val	Met	Gln	Asp	Gly	Thr	Pro	Trp	Pro	Gly	Asn	Asn	Thr	Gly	Asp	465	470	475
His	Pro	Gly	Met	Ile	Gln	Val	Phe	Leu	Gly	Gln	Asn	Gly	Gly	Leu	Asp	485	490	495
Ala	Glu	Gly	Asn	Glu	Leu	Pro	Arg	Leu	Val	Tyr	Val	Ser	Arg	Glu	Lys	500	505	510
Arg	Pro	Gly	Phe	Gln	His	His	Lys	Lys	Ala	Gly	Ala	Met	Asn	Ala	Leu	515	520	525
Val	Arg	Val	Ser	Ala	Val	Leu	Thr	Asn	Gly	Pro	Phe	Ile	Leu	Asn	Leu	530	535	540
Asp	Cys	Asp	His	Tyr	Ile	Asn	Asn	Ser	Lys	Ala	Leu	Arg	Glu	Ala	Met	545	550	555
Cys	Phe	Leu	Met	Asp	Pro	Asn	Leu	Gly	Lys	Gln	Val	Cys	Tyr	Val	Gln	565	570	575
Phe	Pro	Gln	Arg	Phe	Asp	Gly	Ile	Asp	Lys	Asn	Asp	Arg	Tyr	Ala	Asn	580	585	590



09900237 070601

Arg	Asn	Thr	Val	Phe	Phe	Asp	Ile	Asn	Leu	Arg	Gly	Leu	Asp	Gly	Ile	
		595					600					605				
Gln	Gly	Pro	Val	Tyr	Val	Gly	Thr	Gly	Cys	Val	Phe	Asn	Arg	Thr	Ala	
	610					615					620					
Leu	Tyr	Gly	Tyr	Glu	Pro	Pro	Ile	Lys	Val	Lys	His	Lys	Lys	Pro	Ser	
625					630					635					640	
Leu	Leu	Ser	Lys	Leu	Cys	Gly	Gly	Ser	Arg	Lys	Lys	Asn	Ser	Lys	Ala	
				645					650						655	
Lys	Lys	Glu	Ser	Asp	Lys	Lys	Lys	Ser	Gly	Arg	His	Thr	Asp	Ser	Thr	
			660					665					670			
Val	Pro	Val	Phe	Asn	Leu	Asp	Asp	Ile	Glu	Glu	Gly	Val	Glu	Gly	Ala	
		675					680					685				
Gly	Phe	Asp	Asp	Glu	Lys	Ala	Leu	Leu	Met	Ser	Gln	Met	Ser	Leu	Glu	
	690					695					700					
Lys	Arg	Phe	Gly	Gln	Ser	Ala	Val	Phe	Val	Ala	Ser	Thr	Leu	Met	Glu	
705					710					715					720	
Asn	Gly	Gly	Val	Pro	Pro	Ser	Ala	Thr	Pro	Glu	Asn	Leu	Leu	Lys	Glu	
				725					730					735		
Ala	Ile	His	Val	Ile	Ser	Cys	Gly	Tyr	Glu	Asp	Lys	Ser	Asp	Trp	Gly	
			740					745					750			
Met	Glu	Ile	Gly	Trp	Ile	Tyr	Gly	Ser	Val	Thr	Glu	Asp	Ile	Leu	Thr	
		755					760					765				
Gly	Phe	Lys	Met	His	Ala	Arg	Gly	Trp	Arg	Ser	Ile	Tyr	Cys	Met	Pro	
	770					775					780					
Lys	Leu	Pro	Ala	Phe	Lys	Gly	Ser	Ala	Pro	Ile	Asn	Leu	Ser	Asp	Arg	
785					790					795					800	
Leu	Asn	Gln	Val	Leu	Arg	Trp	Ala	Leu	Gly	Ser	Val	Glu	Ile	Leu	Phe	
				805					810					815		
Ser	Arg	His	Cys	Pro	Ile	Trp	Tyr	Gly	Tyr	Asn	Gly	Arg	Leu	Lys	Phe	
			820					825					830			
Leu	Glu	Arg	Phe	Ala	Tyr	Val	Asn	Thr	Thr	Ile	Tyr	Pro	Ile	Thr	Ser	
		835					840					845				
Ile	Pro	Leu	Leu	Met	Tyr	Cys	Thr	Leu	Leu	Ala	Val	Cys	Leu	Phe	Thr	
	850					855					860					
Asn	Gln	Phe	Ile	Ile	Pro	Gln	Ile	Ser	Asn	Ile	Ala	Ser	Ile	Trp	Phe	
865					870					875					880	
Leu	Ser	Leu	Phe	Leu	Ser	Ile	Phe	Ala	Thr	Gly	Ile	Leu	Glu	Met	Arg	
				885				890						895		
Trp	Ser	Gly	Val	Gly	Ile	Asp	Glu	Trp	Trp	Arg	Asn	Glu	Gln	Phe	Trp	
			900					905					910			

Val Ile Gly Gly Val Ser Ala His Leu Phe Ala Val Phe Gln Gly Ile  
 915 920 925  
 Leu Lys Val Leu Ala Gly Ile Asp Thr Asn Phe Thr Val Thr Ser Lys  
 930 935 940  
 Ala Ser Asp Glu Asp Gly Asp Phe Ala Glu Leu Tyr Leu Phe Lys Trp  
 945 950 955 960  
 Thr Thr Leu Leu Ile Pro Pro Thr Thr Leu Leu Ile Val Asn Leu Val  
 965 970 975  
 Gly Val Val Ala Gly Val Ser Tyr Ala Ile Asn Ser Gly Tyr Gln Ser  
 980 985 990  
 Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe Ala Phe Trp Val Ile Val  
 995 1000 1005  
 His Leu Tyr Pro Phe Leu Lys Gly Leu Met Gly Arg Gln Asn Arg Thr  
 1010 1015 1020  
 Pro Thr Ile Val Val Val Trp Ser Val Leu Leu Ala Ser Ile Phe Ser  
 1025 1030 1035 1040  
 Leu Leu Trp Val Arg Ile Asp Pro Phe Thr Ser Arg Val Thr Gly Pro  
 1045 1050 1055  
 Asp Ile Leu Glu Cys Gly Ile Asn Cys  
 1060 1065